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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:36:38 ; Search time 48.9541 Seconds
(without alignments)
249.264 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964

Sequence: 1 MLOMAGOCSONEYFDSLHA.....CKSLPAALSAETIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	4	US-09-565-423-11
2	950	98.5	181	4	US-09-854-864-5
3	572	59.3	185	4	US-09-565-423-17
4	572	59.3	185	4	US-09-854-864-11
5	323	33.5	58	4	US-09-854-864-21
6	311.5	32.3	117	4	US-09-854-864-12
7	286	29.7	283	4	US-09-854-864-9
8	284	29.5	51	4	US-09-854-864-6
9	201	20.9	34	4	US-09-854-864-7
10	201	20.9	81	4	US-09-854-864-13
11	187	19.4	281	4	US-09-854-864-10
12	104	10.8	21	4	US-09-854-864-8
13	79.5	8.2	1009	2	US-08-357-642A-1
14	79.5	8.2	1009	2	US-08-460-626-1
15	78.5	8.1	293	2	US-08-810-572A-2
16	78.5	8.1	293	3	US-09-230-333-2
17	78.5	8.1	293	4	US-09-782-857A-2
18	78.5	8.1	293	4	US-09-879-919-22
19	78.5	8.1	293	4	US-09-848-295-4
20	78.5	8.1	293	4	US-09-854-864-14
21	76	7.9	744	1	US-08-179-481F-2
22	75	7.8	857	1	US-07-717-331F-2
23	73.5	7.6	307	4	US-09-583-110-2671
24	71.5	7.4	835	4	US-09-489-019A-8740
25	71	7.4	333	4	US-09-328-352-6022
26	70.5	7.3	154	3	US-09-232-160-18
27	70.5	7.3	397	4	US-09-854-864-18

28	70	7.3	180	4	US-09-780-717-11	Sequence 11, Appl
29	70	7.3	182	4	US-09-780-717-44	Sequence 44, Appl
30	69.5	7.2	59	4	US-09-854-864-20	Sequence 20, Appl
31	69.5	7.2	166	3	US-08-810-572A-6	Sequence 6, Appl
32	69.5	7.2	166	3	US-09-290-333-6	Sequence 6, Appl
33	69.5	7.2	166	4	US-09-782-857A-6	Sequence 6, Appl
34	69.5	7.2	166	4	US-09-854-864-15	Sequence 15, Appl
35	69.5	7.2	217	4	US-09-252-991A-30641	Sequence 30641, A
36	69.5	7.2	224	4	US-09-465-901-30	Sequence 30, Appl
37	69.5	7.2	353	4	US-09-328-352-5429	Sequence 5429, Ap
38	69.5	7.2	942	4	US-09-695-481-2	Sequence 2, Appl
39	69.5	7.2	1043	4	US-09-695-481-6	Sequence 6, Appl
40	69.5	7.2	1180	3	US-08-560-148-2	Sequence 2, Appl
41	69.5	7.2	1212	3	US-08-660-148-5	Sequence 5, Appl
42	69.5	7.2	1212	4	US-09-695-481-7	Sequence 7, Appl
43	69.5	7.2	1706	2	US-08-459-568-2	Sequence 2, Appl
44	69.5	7.2	1706	2	US-08-399-411-2	Sequence 2, Appl
45	69.5	7.2	1706	3	US-08-516-859A-2	Sequence 2, Appl
46	69.5	7.2	1706	3	US-09-586-472-2	Sequence 2, Appl
47	69.5	7.2	1706	4	US-09-528-706-2	Sequence 2, Appl
48	69.5	7.2	2496	3	US-09-125-028-2	Sequence 2, Appl
49	69.5	7.2	2958	3	US-08-894-344C-2	Sequence 2, Appl
50	69	7.2	324	2	US-08-579-940-7	Sequence 7, Appl
51	69	7.2	445	1	US-08-353-400-33	Sequence 33, Appl
52	69	7.2	447	6	5455030-1	Patent No. 5455030
53	69	7.2	464	1	US-08-353-400-36	Sequence 36, Appl
54	69	7.2	599	1	US-08-442-542-18	Sequence 18, Appl
55	69	7.2	599	3	US-08-765-469-18	Sequence 18, Appl
56	68.5	7.1	228	4	US-09-107-532A-3896	Sequence 3896, Ap
57	68.5	7.1	235	3	US-08-651-136C-8	Sequence 8, Appl
58	68.5	7.1	235	3	US-09-229-911A-8	Sequence 8, Appl
59	68.5	7.1	409	4	US-09-538-092-1214	Sequence 1214, Ap
60	68.5	7.1	877	1	US-08-072-574-12	Sequence 12, Appl
61	68.5	7.1	877	1	US-08-486-270-12	Sequence 12, Appl
62	68.5	7.1	877	3	US-08-367-264-12	Sequence 12, Appl
63	68.5	7.1	877	3	US-09-153-757-12	Sequence 12, Appl
64	68.5	7.1	877	4	US-09-459-715-12	Sequence 12, Appl
65	68.5	7.1	1180	1	US-08-072-574-8	Sequence 8, Appl
66	68.5	7.1	1180	1	US-08-486-270-8	Sequence 8, Appl
67	68.5	7.1	1180	3	US-08-367-264-8	Sequence 8, Appl
68	68.5	7.1	1180	4	US-09-153-757-8	Sequence 8, Appl
69	68.5	7.1	1180	4	US-09-459-715-8	Sequence 8, Appl
70	68.5	7.1	1212	1	US-08-072-574-10	Sequence 10, Appl
71	68.5	7.1	1212	1	US-08-486-270-10	Sequence 10, Appl
72	68.5	7.1	1212	3	US-08-367-264-10	Sequence 10, Appl
73	68.5	7.1	1212	4	US-09-153-757-10	Sequence 10, Appl
74	68.5	7.1	1212	4	US-09-459-715-10	Sequence 10, Appl
75	68	7.1	317	2	US-08-466-337A-18	Sequence 18, Appl
76	68	7.1	317	2	US-08-475-359-18	Sequence 18, Appl
77	68	7.1	317	3	US-08-465-887A-18	Sequence 18, Appl
78	67.5	7.0	178	1	US-08-825-891-1	Sequence 1, Appl
79	67.5	7.0	297	4	US-09-548-130-6	Sequence 6, Appl
80	67.5	7.0	799	1	US-08-188-228-42	Sequence 42, Appl
81	67.5	7.0	799	1	US-08-332-638-42	Sequence 42, Appl
82	67	7.0	182	3	US-09-045-632-29	Sequence 29, Appl
83	67	7.0	283	3	US-09-045-632-27	Sequence 27, Appl
84	67	7.0	310	3	US-08-651-136C-22	Sequence 22, Appl
85	67	7.0	310	3	US-09-329-911A-22	Sequence 22, Appl
86	67	7.0	320	2	US-08-579-940-8	Sequence 8, Appl
87	67	7.0	489	4	US-08-190-204-2	Sequence 2, Appl
88	67	7.0	489	5	PCT-US93-11110-1	Sequence 1, Appl
89	67	7.0	498	6	5221789-1	Patent No. 5221789
90	67	7.0	498	3	US-09-045-632-30	Sequence 30, Appl
91	67	7.0	502	3	US-09-045-632-24	Sequence 24, Appl
92	67	7.0	541	3	US-09-045-632-36	Sequence 36, Appl
93	67	7.0	599	3	US-09-045-632-28	Sequence 28, Appl
94	67	7.0	602	3	US-09-045-632-20	Sequence 20, Appl
95	67	7.0	609	2	US-08-716-301-4	Sequence 4, Appl
96	67	7.0	642	3	US-09-045-632-35	Sequence 35, Appl
97	67	7.0	702	3	US-09-045-632-15	Sequence 15, Appl
98	67	7.0	818	3	US-09-045-632-25	Sequence 25, Appl
99	67	7.0	861	3	US-09-045-632-34	Sequence 34, Appl
100	67	7.0	918	3	US-09-045-632-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
 US-09-565-423-11
 ; Sequence 11, Application US/09565423
 ; Patent No. 6475987
 ; GENERAL INFORMATION:
 ; APPLICANT: SHU, Hong-Bing
 ; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
 ; FILE REFERENCE: 2879-72
 ; CURRENT APPLICATION NUMBER: US/09/565,423
 ; CURRENT FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: UNKNOWN
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/132,892
 ; PRIOR FILING DATE: 1999-05-06
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-565-423-11

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.8e-104;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
 DB 1 MLAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLE 120
 QY 121 YVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 2
 US-09-854-864-5
 ; Sequence 5, Application US/09854864
 ; Patent No. 6774106
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: BLYS/AGP-3, AND TACI
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 181
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-864-5

Query Match 98.5%; Score 950; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 4e-102;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 63
 DB 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 60
 QY 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 123
 DB 61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 120
 QY 124 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
 DB 121 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
 QY 184 R 184
 DB 181 R 181

RESULT 3
 US-09-565-423-17
 ; Sequence 17, Application US/09565423
 ; Patent No. 6475987
 ; GENERAL INFORMATION:
 ; APPLICANT: SHU, Hong-Bing
 ; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
 ; FILE REFERENCE: 2879-72
 ; CURRENT APPLICATION NUMBER: US/09/565,423
 ; CURRENT FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: UNKNOWN
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/132,892
 ; PRIOR FILING DATE: 1999-05-06
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-565-423-17

Query Match 59.3%; Score 572; DB 4; Length 185;
 Best Local Similarity 62.6%; Pred. No. 3.1e-58;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
 QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 63
 DB 1 MAQCFFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKGTVTLWIFLGLT 58
 QY 64 LIISLAVFVLMFLLRKISSEPLKDEFKN---TGSLGGMANIDLEKSRGTDEIILPRGL 119
 DB 59 LVLSLALFTISFLRKNNPEALKDEPQSGQLDGAQDKAOTELTRAGDDRIPRSL 118
 QY 120 EYVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 DB 119 EYVTECTCEDCVKSPKGDSDHFFPLPAMEGATILVTTKTGDKGSSVPTALQSVWGM 178
 QY 178 EKSISAR 184
 DB 179 EKPTHTR 185

RESULT 4
 US-09-854-864-11
 ; Sequence 11, Application US/09854864
 ; Patent No. 6774106
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 59.3%; Score 572; DB 4; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.1e-58;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
Qy 4 MAGCQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAQCQPHSEYFDSLHACKPCRLCSN--PPATCQPCDPSVTSSVKGTTVLMWIFLGLT 58
Qy 64 LIISLAVFVLMFLRLKISSEPLKDFKN-----TCSGLLGHANIDLEKSRGTGDEILPRGL 119
Db 59 LVLISLALFTISFLRKNPALKDQPSQGLDGSQAQLDKADTELTRIRAGDDRIFFPSL 118
Qy 120 EYTVBECTCDDCKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVBECTCDDCKSKPKGSDHDFPLPAMEEGATILVTTKTNDYCKSGSVPTALQSVGM 178
Qy 178 EKSISAR 184
Db 179 EKPTHTR 185

RESULT 5

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 33.5%; Score 323; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CSQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLSLI 65
Db 1 CSQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLSLI 58

RESULT 6

US-09-854-864-12
; Sequence 12, Application US/09854864

; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 32.3%; Score 311.5; DB 4; Length 117;
Best Local Similarity 61.5%; Pred. No. 2.7e-28;
Matches 96; Conservative 4; Mismatches 7; Indels 49; Gaps 19;
Qy 9 SQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLSLI 68
Db 2 AQCEYFDSLHAC-PC-LRCS-----PPTCQ-YC--SVT-SVKGT---LW--LGL---LSL 43
Qy 69 AVFVLMFLRLKISSEPLKDFKN-----TCSGLLGHANIDLEKSRGTGDEILPRGLEYTVECTC 128
Db 44 A-----FPLRLK-----ELKDE-----GSLAL-----RGD---IPR-LEYTVECTC 76
Qy 129 EDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDY 164
Db 77 EDC-KSKPK-DSDH-FPLPAMEEGATILVTTKT-DY 108

RESULT 7

US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 29.7%; Score 286; DB 4; Length 283;
Best Local Similarity 37.6%; Pred. No. 8.8e-25;
Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;
Qy 4 MAGCQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAGCQNEYFDSLHACIPQCRCSSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLS 51
Qy 64 LIISLAVFVLMFLRLKISSEPLKDFKN-----TCSGLLGHANIDLEKSRGTG 110
Db 52 -----GGGGDKTHCTPCPAPPELLGGSVFLFPKPK 84

Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34

RESULT 10
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 20.9%; Score 201; DB 4; Length 81;
Best Local Similarity 100.0%; Pred.No.1.le-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 41
|||
Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34

RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 19.4%; Score 187; DB 4; Length 281;
Best Local Similarity 29.8%; Pred.No.2.7e-13;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

QY 4 MAGQCQSEYFDSLHACIPCOLRCSNTPLTCQRYCNASVTNSVKGNTAILWTCIGLS 63
|||
Db 1 MAQCQFSEYFDSLHACIPCHLRCSN--PPATCQPYCDPSVTSSVKGS----- 47
|||

QY 64 LIISLAVFLMFLLRKISSLEPKDEFNVTGSG-----LLGMANIDLEKSR 108
|||
Db 48 -----YTGGGGGDKTHTCCPPCAPPELLGGPVSFLFPFK 80
|||

OY 109 TGDIEILPRGLEYTVBECTCEDCIKSPKVDSD-----HCFPLPAMEE-----GAT 154


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Db 81 PKDTLMSRTEVTVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 137
Qy 155 ILVTTKNDY-----CKSLPAALSATEIEKTS 182
Db 138 SVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 171

RESULT 12
US-09-854-864-8
; Sequence 8, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-8

Query Match 10.8%; Score 104; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ILWTCGLGLSLIISLAVFLVLMF 75
Db 1 ILWTCGLGLSLIISLAVFLVLMF 21

RESULT 13
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; APPLICATION DATE:
; ATTORNEY/AGENT INFORMATION:

US-08-357-642A-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-357-642A-1

Query Match 8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

Qy 88 EFKNYSGLLGMANIDLEKSR-----TGDEIILPRGLEVTVECTCSDCIKSPKV 138
Db 249 KFFNT---LAGFANIDQETVRCELIQGNWITVDLVIGPKGIQLTSDAKPTCLAEFKQI 305

Qy 139 DSDHCPLPAMERGATIL 156
Db 306 RSIRCLPL---ERQAVL 320

RESULT 14
US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-626-1

Query Match 8.1%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

QY 88 EFKTGGGLGGMANIDLEKSR-----TGDEILLPRGLYTVBECTCEDCIKSPKV 138
DB 249 KFEFT--LAGFANIDQETRYCELIOGNITVDLVIGKGIQLTSQDAKPTCLAEPKQI 305

QY 139 DSDHCFPLPAMEGATIL 156
DB 306 RSIRCLPL---EEQAVL 320

RESULT 15
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-08-810-572A-2

Query Match 8.1%; Score 78.5; DB 2; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKGT--NAILWTCLGLSLI 65
DB 34 CPEQYWDPLLTGTCMCKTICNHQS--QRTCAAFCSLSCKRQKGFYDHLRLDCISCASI 92

QY 66 I-----SLAVFVLMFL-----LRKISSBPLKDFKNTGSGLLGMANIDLEKS-----KVD 107
DB 93 CGQHPKQCAFYFCENKLRSPVNLPPELRRQSRGSEVENNSDNGR--YQGLEHRSSEASPALP 151

QY 108 ---RTGDEILLPRG-----LEVTVEECTCEDCIKSP-----KVD 139
DB 152 GLKLSADQVALVYVSTGLCLCAVLCLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209

QY 140 SDHCFPLPAMEGATILVTTKTINDYC 165
DB 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 16
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 8.1%; Score 78.5; DB 3; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKGT--NAILWTCLGLSLI 65
DB 34 CPEQYWDPLLTGTCMCKTICNHQS--QRTCAAFCSLSCKRQKGFYDHLRLDCISCASI 92

QY 66 I-----SLAVFVLMFL-----LRKISSBPLKDFKNTGSGLLGMANIDLEKS----- 107
DB 93 CGQHPKQCAFYFCENKLRSPVNLPPELRRQSRGSEVENNSDNGR--YQGLEHRSSEASPALP 151

Qy 108 ---RTGDEIILPRG-----LETVBECTCEDCIKXP-----KVD 139
Db 152 GLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209
Qy 140 SDHCFFLPAMEEGATILVTTKTNDYC 165
Db 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 17

US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 8.1%; Score 78.5; DB 4; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

Qy 8 CSONEYFDSLHACIPQLRCSSNTPLTCORYCNASVTSVKGT--NAILWTCGLGLSLI 65
Db 34 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCSRSLSCRKEQKGYDHLRLDCISCASI 92
Qy 66 I-----SLAVFLMFL-----LRKISSEPLKDFKNTGSGLLGMANIDLEKS----- 107
Db 93 CGQHPKQCAFCENKLRSPVNLPPELRRQSRGEVNNSDNSGR-YQGLEHRGSEASPALP 151

Qy 108 ---RTGDEIILPRG-----LETVBECTCEDCIKXP-----KVD 139
Db 152 GLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209
Qy 140 SDHCFFLPAMEEGATILVTTKTNDYC 165
Db 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 18

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-879-919-22

Query Match 8.1%; Score 78.5; DB 4; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

Qy 8 CSONEYFDSLHACIPQLRCSSNTPLTCORYCNASVTSVKGT--NAILWTCGLGLSLI 65
Db 34 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCSRSLSCRKEQKGYDHLRLDCISCASI 92
Qy 66 I-----SLAVFLMFL-----LRKISSEPLKDFKNTGSGLLGMANIDLEKS----- 107
Db 93 CGQHPKQCAFCENKLRSPVNLPPELRRQSRGEVNNSDNSGR-YQGLEHRGSEASPALP 151
Qy 108 ---RTGDEIILPRG-----LETVBECTCEDCIKXP-----KVD 139
Db 152 GLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209
Qy 140 SDHCFFLPAMEEGATILVTTKTNDYC 165
Db 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 19

US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based

GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331P
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-717-331P-2

Query Match 7.8%; Score 75; DB 1; Length 857;
Best Local Similarity 17.6%; Pred. No. 13;
Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

Qy 24 COLRCSNTPLTCQRYCNASVTSVKGTTNAILWT-----58
Db 380 CKKRCISD--CNCTAFANADIRNG--GSGCVIWTRELDIRNYATDAIDGQDLYVRLAA 434
Qy 59 -----CGLSLIISLAVFLMFLRLKISSEPLKDEPKNTGSLGGLGMANIDLEK 106
Db 435 ADIAKKNASGKIISLTGVSLLIMFCL-----WKQKRAKASAIISINTORNO 487
Qy 107 SRTGDEIILPRGLETVVEECTCEDCIKSPKVDSDHCF-----PLPAMEGATILVTTKT 161
Db 488 NLPNMVU-----SSKRFSGEYKFEELPLIEME---TVVKATEN 527
Qy 162 NDYCKSL 168
Db 528 FSSCNKL 534

RESULT 23
US-09-583-110-2671
Sequence 2671, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2671
LENGTH: 307
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-2671

Query Match 7.6%; Score 73.5; DB 4; Length 307;
Best Local Similarity 26.2%; Pred. No. 4.5;
Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

Qy 1 MLOWAGCQSQNEYFDSLHACIPCOLRCSNTPLTCQRYCN-ASVTSVK-GTNAILWT 58
Db 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRLGTSF-FWT 44
Qy 59 CIGLSLI-----ISLAVFLMFLRL-----KISSEPLKDEPKNTGSLGGLGMANIDLE 105
Db 45 LLSITFIGGSMYPMNSIGIIVILLSLTLFKQVRIGTLPSLDEWK-----ANI--E 93
Qy 106 KSRTGDEIILPRGLETVVEECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYC 165
Db 94 SNRLKNKIFIPVML-MAILALVLAQMIPFSKIS-----ISLAAL--PATISVLVITNSHP 146
Qy 166 KSL 168
Db 147 KSL 149

RESULT 24
US-09-489-039A-8740
Sequence 8740, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8740
LENGTH: 835
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8740

Query Match 7.4%; Score 71.5; DB 4; Length 835;
Best Local Similarity 21.0%; Pred. No. 32;
Matches 56; Conservative 36; Mismatches 80; Indels 95; Gaps 14;

Qy 1 MLOWAGCQSQNE-----YFDSLHLHACIP---COL-----RCSNTPLT 36
Db 199 MILMAGFTAGNEKGLVVLGRNGSDYSAAVLAACLRADCCCEIWTVDGVVTCDPQVPP-- 256
Qy 37 CQRYCNASVTSVKGTTNAILWTCLGLSL-----IISLAVFLMFLRLKISSEPL----- 85
Db 257 -----DARLLKMSYQEMELSYFGAKVLPHTPIAQFOIPLCLIKNTGNPOAPGTLIG 311
Qy 86 --KDE-----FKNTGSLGGM-----ANIDLEKSRGTDEIIL--PRGLE 121
Db 312 ASRDEDDLPGKISNLNNMAMFNVSFGMGKMGMAARVATMSRAGISVVLVITQSSEY 371
Qy 122 TVBEECTE-DCIKSPKVDSDHCF-----PLPAMEGATILVTTKTNDYCKSLP--- 169
Db 372 SISFCVPQSDCARAKRAMEDEFYLEKLEPLAIMERLAIISV---VGDGMRLTLAGIS 428
Qy 170 -----AALSATEI-----EKSIS 182
Db 429 AKFFAALARANINIVAIAQSSERSIS 455

[illegible]

Db 76 ATYNWYISNKLQKGGDPF-----A 97

Qy 129 EDCIKSPKVDSDHCFPLPAMEEGATILVTKTNDYCKS---LPAALSAT 175

Db 98 EACLKDCHELYSO-----AIPCLKVDLDDFKDKDYKANIELSAAMEAS 141

RESULT 29

US-09-780-717-44

Sequence 44, Application US/09780717

Patent No. 6713666

GENERAL INFORMATION:

APPLICANT: Helentjaris, Tim

APPLICANT: Bates, Nic

APPLICANT: Allen, Stephen M.

TITLE OF INVENTION: No. 6713666el Invertase Inhibitors and Methods

TITLE OF INVENTION: of Use

FILE REFERENCE: 035719/208677

CURRENT APPLICATION NUMBER: US/09/780,717

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/181,509

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 44

LENGTH: 182

TYPE: PRT

ORGANISM: Glycine max

US-09-780-717-44

Query Match 7.3%; Score 70; DB 4; Length 182;

Best Local Similarity 24.8%; Pred. No. 5.4;

Matches 27; Conservative 23; Mismatches 51; Indels 8; Gaps 2;

Qy 77 LRKISSPLKDFKNTGSLGGMANIDLEKSRGTGDEI--ILPRGLEVTVECTEDCIKS 134

Db 53 IQYLSDDPRSTEADVTGLALIMVNIKANNALDKIHLQKNPEPSQKEPLSSCAARY 112

Qy 135 KPKVDSDHCFPLPAMEEGATILVTKTNDYCKSLPAALSATEIEKSISA 183

Db 113 KAIVEADVAQVASLQKQDPKFAEDGAND-----NAIEATTCSNFSFA 155

RESULT 30

US-09-854-864-20

Sequence 20, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 59

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-20

Query Match 7.2%; Score 69.5; DB 4; Length 59;

Best Local Similarity 25.0%; Pred. No. 1.2;

Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

Qy 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGT--NAILWTCIGLSLI 65

Db 1 CPBEQYWDPLLTGCMSCCTICNHQS-QRTCAAFCRSLSCRKEQKGYDHLRLDCISCASI 59

RESULT 31

US-08-810-572A-6

Sequence 6, Application US/08810572A

Patent No. 5969102

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

APPLICANT: von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

STREET: Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-6

Query Match 7.2%; Score 69.5; DB 2; Length 166;

Best Local Similarity 25.0%; Pred. No. 5.4;

Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

Qy 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGT--NAILWTCIGLSLI 65

Db 34 CPBEQYWDPLLTGCMSCCTICNHQS-QRTCAAFCRSLSCRKEQKGYDHLRLDCISCASI 92

RESULT 32

US-09-290-333-6

Sequence 6, Application US/09290333

Patent No. 6316222

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

APPLICANT: von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30641
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30641

Query Match 7.2%; Score 69.5; DB 4; Length 217;
Best Local Similarity 25.7%; Pred. No. 8;
Matches 29; Conservative 11; Mismatches 46; Indels 27; Gaps 4;
QY 22 IPCQLRCSNTPPLTCQRYCNASVTSVKGNTAILWTCLGLSLIISLAVFLMFLMRKIS 81
DB 124 INCPNASFSQTPAWVCWSSCSRSITQVPGNSLIL---VG-----A 161
QY 82 SEPLKDBFKMTGS-----GLLGMANIDLEKSRGTGDEIILPRGLEVTVECTCED 130
DB 162 REPITITTCSTGSAASAGAENAKRDRESARGAGRGKMGMR-RFPSCCCFD 213

RESULT 36

US-09-465-901-30
; Sequence 30, Application US/09465901
; Patent No. 6492143

GENERAL INFORMATION:

; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-30

Query Match 7.2%; Score 69.5; DB 4; Length 224;
Best Local Similarity 26.4%; Pred. No. 8.4;
Matches 34; Conservative 16; Mismatches 50; Indels 29; Gaps 7;

QY 8 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTSVKGNTAILWTCLGLSLII 66
DB 106 CGPNEIHFTCH-----VPLP-LKLACGENVLEKVGVEIVCITALLGCFLLI 152
QY 67 SLA-VFLMFLMRKISSEPLKDBFKNTGSL-----LGMANIDL-----EKSRGTGDEII 114
DB 153 LLSYAFIVVTILKIPSAEGRHKAFSTCASHLTVVVHYGFASVYILKPKGPKSLEGDTLM 212
QY 115 LPRGLEVTY 123
DB 213 ---GITYTV 218

RESULT 37

US-09-328-352-5429

; Sequence 5429, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5429
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5429

Query Match 7.2%; Score 69.5; DB 4; Length 353;
Best Local Similarity 22.0%; Pred. No. 16;
Matches 35; Conservative 28; Mismatches 63; Indels 33; Gaps 6;
QY 40 YCNASVTSVKGNTAILWTCLGLSLIISLAVFLMFLMRKISSEPLKDBFKNTGSGLLGM 99
DB 3 YC-----AVKNSKSLMHVLSMSILLSL-----SSTPAELVNNPSSGSTGT 44
QY 100 ANIDLEKSRGTG-----DEIILPRG---LEYTVECTCEDCIKSKPKV-----DSDHCFPL 146
DB 45 ASLWSAADAASQLNDEDEDEPTQGSTSVTTILRGSNAPRVITSAPKVPAPIRDTVGYNQA 104
QY 147 PAMEEGATILVTTKTND--YCKSLPAALSATELEKISIA 183
DB 105 PSVSARAALVMDAQOTGEVLYSKNTNASVPISATIKLMTA 143

RESULT 38

US-09-695-481-2
; Sequence 2, Application US/09695481
; Patent No. 6534287

GENERAL INFORMATION:

; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHANN, LAURA
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NPS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-695-481-2

Query Match 7.2%; Score 69.5; DB 4; Length 942;
Best Local Similarity 24.8%; Pred. No. 65;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;
QY 8 CSONEY-FDSLHACIPCOLRCSNTPPLTCQRYCNASVTSVKGNTN-----AILWTCLG 61
DB 537 CXENEIVFVB--YTCACQLG-SWPTDDLT--GCGLIPVOYLRWGDPEPIAAVAVFACLG 590
QY 62 LSLIISLAVFLMFLLR-----KISSEPLKDBFKNTGSGLLGMANIDLEKSRGTGDEIILP 116
DB 591 --LLATLFTVTVFIIYRDTFVVKSSREL-----YIIL 622
QY 117 RGLLEYTVEEC---TCEDCIKSKPKVSDHCF-----PLPAMEEGATILVTTKTN--- 162
DB 623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIIGIGLSPAMYSALV---TKTNRIAR 671

```
QY 163 -----DYCKSLPAALSA 174
Db 672 ILAGSKKIKCTKKPRFMSA 690

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,148
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-148-2

Query Match 7.2%; Score 69.5; DB 3; Length 1180;
Best Local Similarity 24.8%; Pred. No. 90;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSONEY-FDSLHACIPQLCRSSNTPPLTCQRYCNASVTNSVKGTN-----AILWTCLG 61
Db 537 CKENEYVFDE--YTKACQLG-SWPTDDLTLT---GCDLIPQVYLRWGDPEPIAAVVFACLG 590
QY 62 LSLIISLAVFVLMFLRL-----KISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILP 116
Db 591 --LLATLFTVVFIIYRDTPVKSSREL-----YIIL 622
QY 117 RGLTYTVEEC---TCEDCIKSPKVDSDHCF-----PLPAMEGATILVTTKTN--- 162
Db 623 AGI-----CLGYLCTFLIAKPK--QIYCYLQRIQIGLSPAMSYSALV---TKTNRIAR 671
QY 163 -----DYCKSLPAALSA 174
Db 672 ILAGSKKIKCTKKPRFMSA 690

RESULT 41
US-08-660-148-5
; Sequence 5, Application US/08660148
; Patent No. 6211353
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;

QY 163 -----DYCKSLPAALSA 174
Db 672 ILAGSKKIKCTKKPRFMSA 690

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/695,481
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/695,481
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORMANN, THOMAS M.
; REGISTRATION NUMBER: 1094.2.6
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric
; US-09-695-481-6

Query Match 7.2%; Score 69.5; DB 4; Length 1043;
Best Local Similarity 24.6%; Pred. No. 75;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSONEY-FDSLHACIPQLCRSSNTPPLTCQRYCNASVTNSVKGTN-----AILWTCLG 61
Db 537 CKENEYVFDE--YTKACQLG-SWPTDDLTLT---GCDLIPQVYLRWGDPEPIAAVVFACLG 590
QY 62 LSLIISLAVFVLMFLRL-----KISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILP 116
Db 591 --LLATLFTVVFIIYRDTPVKSSREL-----YIIL 622
QY 117 RGLTYTVEEC---TCEDCIKSPKVDSDHCF-----PLPAMEGATILVTTKTN--- 162
Db 623 AGI-----CLGYLCTFLIAKPK--QIYCYLQRIQIGLSPAMSYSALV---TKTNRIAR 671
QY 163 -----DYCKSLPAALSA 174
Db 672 ILAGSKKIKCTKKPRFMSA 690

RESULT 40
US-08-660-148-2
; Sequence 2, Application US/08660148
; Patent No. 6211353
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/695,481
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/695,481
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORMANN, THOMAS M.
; REGISTRATION NUMBER: 1094.2.6
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric
; US-09-695-481-6
```

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Db      537 CKENEYVFDE--YTKACKQLG-SWPTDDLT---CCDLIPVOYLKRWGDEPTAAVVFACLG 590
Qy      62  LSLHISLAVFVLMFLLR-----KISSPCLKDEFKNTGSLGLGMANIDLEKSRGTGEIILP 116
Db      591 --LLATLFVTWVFIYRDTPWVKSSREL-----YIIL 622
Qy      117 RGLSYTVBEC---TCBDCIKSKPKVSDHCF-----PLPAMEGATILVTTKTN----- 162
Db      623 AGI-----CLGYLCTCLIAKPK--QIYCYLQIRIGISLSPAMSALV---TKTNRIAR 671
Qy      163 -----DYCKSLPALSA 174
Db      672 ILAGSKKKICTKRPFMSA 690

RESULT 43
US-08-459-568-2
; Sequence 2, Application US/08459568
; Patent No. 581304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-568-2

Query Match 7.2%; Score 69.5; DB 2; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7

Qy      34  PLTCQRYCNASVTNSVKGTTNAILWTCLGLSLIISLAVFLMFLLRKISSEPLKDEFKNTG 93
Db      598 PVTVE-----ITQNIKSTQV-----SVTDDLKDSPSST- 626
Qy      94  SGLLGMANIDLEKSRGTGEIILPRGLSYTVBECTCEDCIKSKP-----KVDSHCFFLP 147
Db      627 -----NCSEKKRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH----- 674
Qy      148 AMEGATILVTTKNDYCK-----SLPAALSATEIEK 179
Db      675 -KEKG--VYLLSKKLQQLQTKLTLFAGSAAEIPK 708

```

5

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-586-472-2

Query Match 7.2%; Score 69.5; DB 3; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

Qy 34 PLTCQRYCNASVTVNSVKGTHAILWTCIGLSLIISLAVFLVLMFLLRKISSPLKDEPKNTG 93
Db 598 PVTVE-----ITQNIKSTQV-----SVTDDLKXSPSST- 626

Qy 94 SGLLGWANIIDLEKSRGTDEIILPRGLETVVEECTCEDCIKSKP-----KVDSHCHCPPLP 147
Db 627 -----NCSEKKRRRTASPPVLPKIKTETESDSTAPSCSLPLSISTABVVSFH----- 674

Qy 148 AMEGATILVTTKNDYCK-----SLPAALSATEIEK 179
Db 675 -KEKG--VYLSSKQLQQLQDQKLTLPAGSAAEIPK 708

RESULT 47
US-09-528-706-2
; Sequence 2, Application US/09528706
; Patent No. 646895
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683

; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-528-706-2

Query Match 7.2%; Score 69.5; DB 4; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

Qy 34 PLTCQRYCNASVTVNSVKGTHAILWTCIGLSLIISLAVFLVLMFLLRKISSPLKDEPKNTG 93
Db 598 PVTVE-----ITQNIKSTQV-----SVTDDLKXSPSST- 626

Qy 94 SGLLGWANIIDLEKSRGTDEIILPRGLETVVEECTCEDCIKSKP-----KVDSHCHCPPLP 147
Db 627 -----NCSEKKRRRTASPPVLPKIKTETESDSTAPSCSLPLSISTABVVSFH----- 674

Qy 148 AMEGATILVTTKNDYCK-----SLPAALSATEIEK 179
Db 675 -KEKG--VYLSSKQLQQLQDQKLTLPAGSAAEIPK 708

RESULT 48
US-09-125-028-2
; Sequence 2, Application US/09125028A
; Patent No. 6190707
; GENERAL INFORMATION:
; APPLICANT: WADOUX, Isabelle
; APPLICANT: COLAVIZZA, Didier
; APPLICANT: LOJEAZ, Annie
; TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
; FILE REFERENCE: levure sensible froid
; CURRENT APPLICATION NUMBER: US/09/125,028A
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: PCT/FR97/00254
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2496
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-125-028-2

Query Match 7.2%; Score 69.5; DB 3; Length 2496;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
Matches 34; Conservative 17; Mismatches 49; Indels 37; Gaps 5;

Qy 66 ISLAVFLVLMFLLRKISSPLKDE-----FKYTGSGLLGHANIDL----- 104
Db 1219 ILLDVDFLLFIFAKSLLEQLYSENWVQLDDIEIGIVKRLSNLQEGITSINIDIIHAYL 1278
Qy 105 -----EKSRTGDEIILPRGLETVVEECTCEDCIKSKPKVDSHCHFPPLPAMEEGATILVTT 159
Db 1279 NLIWQETGEGFEYLYDR-IDYQMS-----KSLKQRTNKLLLEVALAKVTVRTV 1330
Qy 160 ---KTNDYCKSLPAALS 173
Db 1331 NQKNPDLSEDRPPALS 1347

RESULT 49
```

US-08-894-344C-2
; Sequence 2, Application US/08894344C
; Patent No. 6172196
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, Hideki
; APPLICANT: TOKAI, Masaya
; APPLICANT: KIKUCHI, Yasuhiro
; APPLICANT: OUCHI, Kozo
; TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING
; TITLE OF INVENTION: YEAST
; TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: FITZPATRICK, CELIA, HARPER & SCINTO
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS Ver3.30
; SOFTWARE: PATENT AID Ver1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894.344C
; FILING DATE: 15-AUGUST-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP343700/95
; FILING DATE: 28-DECEMBER-1995
; APPLICATION NUMBER: PCT/JP96/03862
; FILING DATE: 27-DECEMBER-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perty, Lawrence S.
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-218-2100
; TELEFAX: 212-218-2200
; INFORMATION FOR SEQ ID NO: 2 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2958 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; STRAIN: X2180-1B
US-08-894-344C-2

Query Match 7.2%; Score 69.5; DB 3; Length 2958;
Best Local Similarity 24.8%; Pred. No. 3.4e+02;
Matches 34; Conservative 17; Mismatches 49; Indels 37; Gaps 5;
Qy 66 ISLAVFLMFLLRKISSPLKDE-----FKVTGSLGGMANIDL----- 104
Db 1219 ILLDVPDLFFIFAKSLLEQLYSENVMVQLDDIEIGIVKRLSNLQEGTISNIDIHAYL 1278
Qy 105 -----EKSRGTDEIILPRGLYTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTT 159
Db 1279 NLIWQETGEGFELYLDR-IDYQSE-----KSLEKRTNKLLEVAALAKVTVTVTV 1330
Qy 160 ---KTNDYCKSLPAALS 173
Db 1331 NQKNPDLSEDRPPALS 1347

RESULT 50

US-08-579-940-7
; Sequence 7, Application US/08579940
; Patent No. 5977315
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Kohler, Heinz

; APPLICANT: Poon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; TITLE OF INVENTION: 3H1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,940
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 30414-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-940-7
Query Match 7.2%; Score 69; DB 2; Length 324;
Best Local Similarity 36.0%; Pred. No. 16;
Matches 18; Conservative 9; Mismatches 15; Indels 8; Gaps 2;
Qy 111 DEILPRGLYTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTK 160
Db 94 DKKIVPR-----DCGCKPCICTVPEVSVFIFP-PKPKDVLITLITPK 135
Search completed: January 28, 2005, 19:48:39
Job time : 50.9541 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:37:53 ; Search time 36.3395 Seconds
(without alignments)
335.635 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201
Sequence: 1 CSQNEVFDLSLLHACIPQLRCSNTPTLCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	34	5	Aae15486 Human B-C
2	201	100.0	34	6	Ada49366 Human BCM
3	201	100.0	51	5	Aae15485 Human B-C
4	201	100.0	58	5	Aae15501 Human B-C
5	201	100.0	181	5	Aae15484 Human B-C
6	201	100.0	184	3	Aab08843 Amino aci
7	201	100.0	184	3	Aay94001 A human B
8	201	100.0	184	4	Aae09241 Human BCM
9	201	100.0	184	4	Aay71979 Human B-C
10	201	100.0	184	4	Aab60698 Human BAF
11	201	100.0	184	4	Aae00506 Human B C
12	201	100.0	184	5	Abb81487 Human BCM
13	201	100.0	184	5	Abp54694 Metastati
14	201	100.0	184	5	Aae28961 Human B-C
15	201	100.0	184	6	Aae35216 Human B-C
16	201	100.0	184	6	Ada49361 Human BCM
17	201	100.0	184	6	AbR40082 Human Gen
18	201	100.0	184	6	Abp60552 Human tum
19	201	100.0	184	6	Abp97717 Amino aci
20	201	100.0	184	7	Adp67527 Human Lyl
21	201	100.0	184	7	Adg43715 Human B-C
22	201	100.0	184	8	Adk00756 Native hu
23	201	100.0	283	5	Aae15488 Human BCM
24	201	100.0	288	5	Abg95060 Human tra
25	201	100.0	302	4	Aab60699 Mouse Irg

26	201	100.0	302	4	Aae00507 Human BCM
27	201	100.0	302	7	Adg43717 Human B-C
28	159.5	79.4	157	4	Aab60700 Human BAF
29	151	75.1	26	7	Adi53060 Human BCM
30	136	67.7	185	3	Aab08844 Amino aci
31	136	67.7	185	4	Aay71980 Murine B
32	136	67.7	185	5	Aae15490 Mouse B C
33	136	67.7	281	5	Aae15489 Mouse BCM
34	124	61.7	42	6	Abj38417 TALL-1 re
35	93.5	46.5	117	5	Aae15491 Human-mur
36	90.5	45.0	24	3	Aay94006 A murine
37	71.5	35.6	249	3	Aae15492 Human-mur
38	67.5	33.6	1548	7	Adc71568 Mouse sub
39	67.5	33.6	1877	7	Abb80243 Murine su
40	66.5	33.1	33	5	Aae15495 Human TAC
41	66.5	33.1	33	6	Ada49368 Human TAC
42	66.5	33.1	37	5	Aau10951 Human AGP
43	66.5	33.1	59	5	Aae15500 Human TAC
44	66.5	33.1	166	2	Aaw75785 Human lym
45	66.5	33.1	166	5	Aae15494 Human TAC
46	66.5	33.1	171	8	Adn03188 Human TAC
47	66.5	33.1	265	4	Aae09244 Human TAC
48	66.5	33.1	266	6	Abp97723 Amino aci
49	66.5	33.1	291	5	Aau10949 Human AGP
50	66.5	33.1	293	2	Aaw75783 Human lym
51	66.5	33.1	293	3	Aay36312 Human neu
52	66.5	33.1	293	3	Aay94000 A transme
53	66.5	33.1	293	4	Aae09240 Human TAC
54	66.5	33.1	293	4	Aay71914 Human tum
55	66.5	33.1	293	5	Aao14130 Human tra
56	66.5	33.1	293	5	Abb81488 Human TAC
57	66.5	33.1	293	5	Aau99512 Human TAC
58	66.5	33.1	293	5	Aae28962 Human TAC
59	66.5	33.1	293	5	Aau75408 Tumour ne
60	66.5	33.1	293	5	Aau09900 Human AGP
61	66.5	33.1	293	5	Aae15493 Human tra
62	66.5	33.1	293	5	Abg71496 Human tum
63	66.5	33.1	293	6	Aae35211 Human TAC
64	66.5	33.1	293	6	Abp60551 Human tum
65	66.5	33.1	293	6	Abp97716 Amino aci
66	66.5	33.1	293	6	Aao29592 Human DIT
67	66.5	33.1	293	7	Adf72628 Human tum
68	66.5	33.1	293	7	Adf77379 Human tum
69	66.5	33.1	293	8	Adk00754 Native hu
70	66.5	33.1	293	8	Adj92514 Human TAC
71	66.5	33.1	293	8	Adn03174 Human TAC
72	66.5	33.1	294	8	Adk00765 hTACI spl
73	66.5	33.1	312	5	Aao14135 Protein o
74	66.5	33.1	332	6	Aae35228 Human TAC
75	66.5	33.1	334	5	Aao14133 Protein o
76	66.5	33.1	344	6	Aae35224 Human TAC
77	66.5	33.1	348	6	Aae35225 Human TAC
78	66.5	33.1	357	6	Aae35226 Human TAC
79	66.5	33.1	366	5	Aao14132 Protein o
80	66.5	33.1	392	6	Aae35223 Human TAC
81	66.5	33.1	397	5	Aae15498 Human TAC
82	66.5	33.1	404	5	Aao14136 Protein o
83	61	30.3	1887	6	Abu12113 Human pro
84	61	30.3	1887	7	Abb80242 Human sub
85	61	30.3	1887	7	Adm29324 Human nov
86	59.5	29.6	138	5	Abp69083 Human pol
87	59.5	29.6	353	4	Abb71555 Drosophil
88	59.5	29.6	418	5	Abb08238 Human 567
89	59.5	29.6	581	7	Adb64650 Human pro
90	59.5	29.6	735	5	Aag68258 Human POL
91	59.5	29.6	735	6	Abu12091 Novel hum
92	59.5	29.6	845	5	Aag68259 Human POL
93	59.5	29.6	845	6	Abu12092 Novel hum
94	59.5	29.6	845	7	Aae38807 Human POL
95	59.5	29.6	880	7	Adb64680 Human pro
96	59.5	29.6	897	4	Aag65887 Amino aci
97	59.5	29.6	897	4	Abg06309 Novel hum
98	59.5	29.6	897	5	Abg91402 Primate L

99 59.5 29.6 897 7 ADE07852 Novel pro
100 59.5 29.6 897 7 ADE08940 Novel pro

ALIGNMENTS

RESULT 1

AAE15486
ID AAE15486 standard; peptide; 34 AA.

XX AAE15486;

DT 12-MAR-2002 (first entry)

XX Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.

XX Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein cysteine-rich consensus region

XX Sequence 34 AA;

Query Match 100.0%; Score 201; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSNTPTPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSNTPTPLTCQRYC 34

RESULT 2

ADA49366

ID ADA49366 standard; peptide; 34 AA.

XX ADA49366;

DT 20-NOV-2003 (first entry)

XX Human BCMA cysteine rich domain.

XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
KW antiarthritic; dermatological; antidiabetic; neuroprotective;
KW antichyroid; antipyretic; nephrotropic; vasotropic; vaccine;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW insulin dependent diabetes mellitus; multiple sclerosis;
KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
KW pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
KW cysteine rich domain.

XX Homo sapiens.

XX WO2003035846-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-03445106P.

XX 14-JAN-2002; 2002US-0348962P.

XX 07-FEB-2002; 2002US-0354966P.

XX 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.

XX Disclosure; Page 616; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting bkg; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. It is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarteritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human BCMA.

CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein extracellular domain

XX

SQ Sequence 51 AA;

Query Match 100.0%; Score 201; DB 5; Length 51;
Best Local Similarity 100.0%; Pred No. 3.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
|||||
Db 5 CSONEYFDSLHACIPQLRCSSTNPPLTCQRYC 38
|||||

RESULT 4
AAE15501
ID AAE15501 standard; peptide; 58 AA.
XX AC
XX AAE15501;
XX DT
XX 12-MAR-2002 (first entry)
XX Human B cell maturation protein cysteine rich extracellular region.

DE Human; transmembrane activator and intracellular CAML interactor; TACI;
KW Cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.
XS WO200187979-A2.
XX 22-NOV-2001.
XX 14-MAY-2001; 2001WO-US015567.
XX 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2000US-00214591.
PA (AMGE-) AMGEN INC.
PI Theill LE, Yu G;
PI WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX Disclosure; Fig 13; 94pp; English.

PS The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region
 XX
 SQ Sequence 58 AA;
 Query Match 100.0%; Score 201; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 RESULT 5
 AAE15484
 ID AAE15484 standard; protein; 181 AA.
 XX
 AC AAE15484;
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B-cell maturation (BCMA) protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cystostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 5..38
 FT /note= "Cysteine-rich consensus region; This is region is
 FT specifically claimed as SEQ ID NO: 7 in claim 1 of the
 FT specification"
 FT 52..72
 FT /label= Transmembrane_domain
 FT WO200187979-A2.
 XX
 PN 22-NOV-2001.
 XX
 PD 14-MAY-2001; 2001WO-US015567.
 XX
 PF 12-MAY-2000; 2000US-0204039P.
 XX
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 PI WPI; 2002-066686/09.
 XX
 DR Inhibiting activity of B cell maturation protein and/or transmembrane
 XX activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 PT
 XX Disclosure; Fig 10A; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC

CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein
 XX
 SQ Sequence 181 AA;
 Query Match 100.0%; Score 201; DB 5; Length 181;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38
 RESULT 6
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 XX
 AC AAB08843;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of human.
 XX
 KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 57..77
 FT /note= "putative transmembrane domain"
 FT WO200050633-A1.
 XX
 PN 31-AUG-2000.
 XX
 PD 24-FEB-2000; 2000WO-US004925.
 XX
 PF 24-FEB-1999; 99US-0121485P.
 XX
 PR (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Ting A;
 XX
 PI WPI; 2000-558405/51.
 XX
 DR Identifying a modulator of gene expression for drug designing, by
 XX contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression.
 PT
 XX Claim 32; Fig 7A; 53pp; English.
 PS
 XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
 CC a necrosis factor (NF)-kB activator. The method of the invention is used
 CC to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease, or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 34

DB 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 41

RESULT 7

AA94001

ID AA94001 standard; protein; 184 AA.

AC AA94001;

DT 20-OCT-2000 (first entry)

DE A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO200040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58559.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used

CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 34

DB 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 41

RESULT 8

AAE09241

ID AAE09241 standard; protein; 184 AA.

AC AAE09241;

DT 19-NOV-2001 (first entry)

DE Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0226986P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;

XX WPI; 2001-541628/60.

XX N-PSDB; AAD15902.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological

PT activity, for treating autoimmune disorders and cancer, comprises

PT exposing the cells to TALL-1 or APRIL polypeptide agonists or

PT antagonists.

XX Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction

CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human BCMA protein

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 34
 |||||
 DB 8 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 41

RESULT 9

ID AAY71979 standard; protein; 184 AA.

AC AAY71979;

DT 28-MAR-2001 (first entry)

DE Human B cell maturation factor (BCMA) protein.

Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

OS Homo sapiens.

Key Location/Qualifiers
 Domain 1..62
 /label= Extracellular_domain

FN WO200068378-A1.

PD 16-NOV-2000.

PF 05-MAY-2000; 2000WO-US012266.

PR 06-MAY-1999; 99US-012892P.

PR 01-MAY-2000; 2000US-0201012P.

PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX N-PSDB; AAD02125.

Isolated TALL-1 protein is used to identify compounds that regulate B
 lymphocyte proliferation, used to treat B lymphocyte associated
 autoimmune disorders.

PS Claim 37; Page 104-105; 112pp; English.

The present invention relates to Tumour necrosis factor (TNF) and Apol-
 related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus

CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA) protein.
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
 CC increases with B lymphocyte maturation

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 34

|||||
 DB 8 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 41

RESULT 10

AAB60698

ID AAB60698 standard; protein; 184 AA.

AC AAB60698;

DT 22-MAY-2001 (first entry)

DE Human BAFF receptor (BAFF-R).

Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

immune-related disorder; B-cell growth inhibitor; BCMA;

B-cell maturation inhibitor; immunoglobulin production inhibitor;

autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

renal disorder; immunosuppressive disorder; HIV infection;

organ transplantation; antiinflammatory; systemic lupus erythematosus;

autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;

B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;

lymphoma; gene therapy; cancer; tumour.

OS Homo sapiens.

PN WO200112812-A2.

PD 22-FEB-2001.

PF 16-AUG-2000; 2000WO-US022507.

PR 17-AUG-1999; 99US-0149378P.

PR 11-FEB-2000; 2000US-0181684P.

PR 18-FEB-2000; 2000US-0183536P.

XX (BIOJ) BIOGEN INC.

XX (APOT-) APOTEC R & D SA.

XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

PI Thompson J;

XX WPI; 2001-202866/20.

XX N-PSDB; AAF59998.

Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.

XX Claim 20; Fig 1; 59pp; English.

The invention relates to the use of a BAFF receptor (BAFF-R, also known
 as BCMA) protein, or a BAFF-R fusion protein as an agent for the

CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAFF-R
 CC
 XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSNTPLTCQRYC 34
 |||||
 DB 8 CSQNEVFDLSLLHACIPQLRCSNTPLTCQRYC 41

RESULT 11

AAE00506
 ID AAE00506 standard; protein; 184 AA.

XX AC AAE00506;

DT 31-JUL-2001 (first entry)

XX DE Human B cell maturation protein (BCMA).

XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;
 KW tumour necrosis factor; BCMA; B cell maturation protein.

XX OS Homo sapiens.

XX PN WO200124811-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US027579.

XX PR 06-OCT-1999; 99US-0157933P.

XX PR 11-FEB-2000; 2000US-0181807P.

XX PR 30-JUN-2000; 2000US-0215688P.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTECH R & D SA.

XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

XX DR N-PSDB; AAD03844.

XX WPI; 2001-266242/27.

XX DR N-PSDB; AAD03844.

PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)

PT antagonist.

XX Claim 3; Fig 3A; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or carcinoma.
 CC The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is human APRIL-R also referred as BCMA or BCM protein

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSNTPLTCQRYC 34
 |||||

DB 8 CSQNEVFDLSLLHACIPQLRCSNTPLTCQRYC 41

RESULT 12

ABB81487

ID ABB81487 standard; protein; 184 AA.

XX AC ABB81487;

XX DT 02-SEP-2002 (first entry)

XX DE Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Tnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX OS Homo sapiens.

XX PN WO200238766-A2.

XX PD 16-MAY-2002.

XX PF 05-NOV-2001; 2001WO-US047018.

XX PR 07-NOV-2000; 2000US-0246449P.

XX PR 20-DEC-2000; 2000US-0257131P.

XX PR 28-JUN-2001; 2001US-0301715P.

XX PR 29-AUG-2001; 2001US-0315565P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Henne RM, Grant FJ;

XX WPI; 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.
 XX
 XX
 PS Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 13
 ABP54694

ID ABP54694 standard; protein; 184 AA.

AC ABP54694;

XX 30-DEC-2002 (first entry)

DE Metastatic colorectal cancer-associated polypeptide.

XX Colorectal cancer; metastasis; differential expression; cytostatic;
 KW diagnosis; gene therapy; vaccine.

XX Homo sapiens.

XX WO200268677-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US006001.

XX 27-FEB-2001; 2001US-027206P.

XX 02-APR-2001; 2001US-0281149P.

XX 17-APR-2001; 2001US-0284555P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Mack DH, Markowitz SD;

XX WPI; 2002-698677/75.

XX N-PSDB; ABQ81560.

XX New genes that are up- or down-regulated in colorectal cancer, useful for
 PT diagnosing colorectal cancer in a subject, or for identifying modulators
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.

XX Claim 8; Page 255; 260pp; English.

XX The present sequence is the protein sequence of a human polypeptide
 CC encoded by a gene that exhibits decreased expression in colon cancer-
 CC derived metastases compared to normal colon tissue. It is an example of
 CC claimed polypeptides that are encoded by genes which are differentially
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are
 CC useful in diagnostic and prognostic assays, for raising antibodies useful
 CC e.g. in immunotherapy, and in screening for modulator compounds of
 CC therapeutic value

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 14

AAE28961

ID AAE28961 standard; protein; 184 AA.

XX AAE28961;

XX 27-JAN-2003 (first entry)

XX Human B-cell maturation antigen (BCMA).

XX Human; tumour; B-cell maturation antigen; transmembrane activator;
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; Gene therapy;
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 KW BCMA; multiple myeloma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..54 /note= "Antigenic epitope"

XX Domain 1..48 /note= "Extracellular domain"

XX Region 8..41 /note= "Cysteine rich region"

XX WO200265516-A2.

XX 29-AUG-2002.

XX 06-FEB-2002; 2002WO-US003500.

XX 20-FEB-2001; 2001US-0270274P.

XX 12-APR-2001; 2001US-0283447P.

XX (ZYMO) ZYMOGENETICS INC.

XX Kindvogel W;

XX WPI; 2002-723183/78.

XX N-PSDB; AAD46410.

XX B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.

XX Disclosure; Page 63; 67pp; English.

XX The invention relates to the manufacture of a composition for inhibiting

CC the proliferation of tumour cells. The method involves using an antibody

CC component that binds both the B-cell maturation antigen (BCMA) and the

CC transmembrane activator and calcium-modulator and cyclophilin ligand-

CC interactor (TACI). BCMA and TACI binding antibody compositions are useful

CC for inhibiting proliferation of tumour cells, particularly inhibiting

CC ZTNF4 activity in a mammal associated with increased endogenous antibody

CC production or a disorder consisting of neoplasm, chronic lymphocytic

CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation

CC lymphoproliferative disease or light chain gammopathy or inflammation

CC e.g. asthma. The invention is also useful in gene therapy. The present is

CC human BCMA protein

XX

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 34

DB 8 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 15

AAE35216

ID AAE35216 standard; protein; 184 AA.

XX

AC AAE35216;

XX

DT 28-MAY-2003 (first entry)

XX

DE Human B-cell maturation receptor (BCMA) protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;

KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;

KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;

KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;

KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;

KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;

KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;

KW B-cell maturation receptor; BCMA; receptor.

XX

OS Homo sapiens.

XX

PN WO200294852-A2.

XX

PD 28-NOV-2002.

XX

PF 20-MAY-2002; 2002WO-US015910.

XX

XX 24-MAY-2001; 2001US-0293343P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Rixon MW, Gross JA;

XX

XX WPI; 2003-148455/14.

DR N-PSDB; AAD53754.

XX

PT Transmembrane activator and calcium modulator and cyclophilin ligand-

PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or

PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

PS Disclosure; Col 100; 71pp; English.

XX

CC The invention relates to fusion proteins comprising transmembrane

CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)

CC receptor group that binds tumour necrosis factor-like protein (ZTNF2 or

CC ZTNF4; and an immunoglobulin group comprising a constant region of an

CC immunoglobulin. The invention is used to manufacture a medicament for

CC inhibiting the proliferation of tumour cells in a mammalian subject. The

CC composition comprising the fusion protein may also be used in treating

CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple

CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft

CC rejection, anaemia and septic shock. The fusion proteins are also used in

CC gene therapy. The present sequence is human B-cell maturation receptor

CC (BCMA) protein used in the invention

XX

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 34

DB 8 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 16

ADA49361

ID ADA49361 standard; protein; 184 AA.

XX

AC ADA49361;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human BCMA protein.

XX

KW human; TALL-1; antagonist; immunosuppressive; antirheumatic;

KW antiinflammatory; antiarthritic; dermatological; antidiabetic;

KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;

KW vaccine; autoimmune disease; rheumatoid arthritis;

KW systemic lupus erythematosus; insulin dependent diabetes mellitus;

KW multiple sclerosis; myasthenia gravis; Grave's disease;

KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;

KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

XX

OS Homo sapiens.

XX

PN WO2003035846-A2.

XX

PD 01-MAY-2003.

XX

PF 24-OCT-2002; 2002WO-US034376.

XX

PR 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX

XX (NAJB-) NAT JEWISH MEDICAL & RES CENT.

XX

PI Zhang G, Shu H, Liu Y, Xu L;

XX

XX WPI; 2003-403345/38.

DR N-PSDB; ADA49360.

XX

PT Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological

PT activity in mammal, has a modification in the region connecting beta

PT strands D and E that reduces the biological activity of TALL-1

PT antagonist.

XX

PS Claim 62; Page 613; 618pp; English.

XX

CC The invention relates to a novel TALL-1 antagonist protein, comprising a

CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID

CC NO:2, by at least one modification in the region connecting E&G; strands

CC D and E that reduces the biological activity of the TALL-1 antagonist as

CC compared to wild-type TALL-1. A protein of the invention has

CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
 |||||

RESULT 17
 ABR40082
 ID ABR40082 standard; protein; 184 AA.
 XX
 XX
 AC ABR40082;
 XX
 XX
 DT 27-JUN-2003 (first entry)
 XX
 XX
 DE Human Genoxit.

XX Human; genoxit; anorectic; antilipaeamic; antiarteriosclerotic; cardiant;
 KW antidiabetic; hypotensive; ophthalmological; neuroprotective; Family;
 KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super
 KW Type III transmembrane protein; insulin resistance; atherosclerosis;
 KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
 KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
 XX
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..54
 FT /label= Extracellular_domain
 FT Misc-difference 3
 FT /label= Gln, Lys
 FT Domain 55..77
 FT /label= Transmembrane_domain
 FT Domain 78..184
 FT /label= Intracellular_domain

XX WO2003013582-A1.
 XX
 XX
 PD 20-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-IB003498.
 XX
 XX 06-AUG-2001; 2001US-0310754P.
 XX
 XX (GENT) GENSET SA.
 XX

XX Lucas J, Dialynas D, Briggs K;
 XX WPI; 2003-268160/26.
 XX N-PSDB; ACC00340.
 XX

XX New use of agonist or antagonist of Genoxit activity for preventing or
 FT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
 FT atherosclerosis.
 XX
 XX
 PS Disclosure; Page 32; 35pp; English.

XX

CC The present invention relates to the use of an agonist or antagonist of
 CC Genoxit activity for preventing or treating obesity. Genoxit is a member
 CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
 CC transmembrane protein. The agonists or antagonists of the invention are
 CC useful for treating or preventing obesity-related diseases or disorders,
 CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
 CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
 CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
 CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
 CC complications, e.g. microangiopathic lesions, ocular lesions,
 CC retinopathy, neuropathy and renal lesions
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
 |||||

RESULT 18
 ABR60552
 ID ABR60552 standard; protein; 184 AA.
 XX
 XX
 AC ABR60552;
 XX
 XX
 DT 28-MAR-2003 (first entry)
 XX
 XX
 DE Human tumour necrosis factor BCMA.

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antineumatic;
 KW antiarthritic; cyostatic; antianaemic; antiallergic; antiasthmatic;
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.
 XX
 XX Homo sapiens.

XX WO200294192-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 22-MAY-2002; 2002WO-US016106.
 XX
 XX 24-MAY-2001; 2001US-0293100P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM;
 XX WPI; 2003-156740/15.

XX Novel isolated antibody that immunospecifically binds tumor necrosis
 FT factor delta, useful for treating, preventing or ameliorating Non-
 FT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 FT syndrome.
 XX
 XX Disclosure; Page 222; 225pp; English.

XX The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiarthritic, cyostatic, antianaemic,
 CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,
 CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or

CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
CC human, disease or disorder such as autoimmune disease, and graft versus
CC host disease (GVHD). The autoimmune disease is systemic lupus
CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
CC is useful for detecting, diagnosing, prognosing, treating, preventing or
CC ameliorating a disease or disorder associated with aberrant APRIL or
CC APRIL receptor expression or aberrant function of APRIL or APRIL
CC receptor. The disease or disorders includes autoimmune and inflammatory
CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
CC system, particularly B cell cancers, immune disorders such as myasthenia
CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
CC proliferative disorders (e.g. leukemia). The present sequence represents
CC the tumour necrosis factor BCMA
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 19
ABP97717
ID ABP97717 standard; protein; 184 AA.

AC ABP97717;
XX
XX 28-MAY-2003 (first entry)

DE Amino acid sequence of human BCMA receptor.

XX Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX TALL-1; April; systemic lupus erythematosus; BCMA.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX N-PSDB; ABZ68871.

XX New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 2; 153pp; English.

XX The present sequence represents a human BCMA polypeptide. The
CC specification also describes TAC1 and BR3 polypeptides. TAC1 and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 20
ADD67527
ID ADD67527 standard; protein; 184 AA.

XX ADD67527;

XX 15-JAN-2004 (first entry)

XX Human Ly1732P protein SEQ ID NO:4.

XX haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
XX vaccine; immunotherapy; cancer; multiple myeloma cell;
XX chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
XX human.

XX Homo sapiens.

XX WO2003062401-A2.

XX 31-JUL-2003.

XX 22-JAN-2003; 2003WO-US002353.

XX 22-JAN-2002; 2002US-00057475.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
XX Carter L, McNeill PD;

XX WPI; 2003-598749/56.

XX N-PSDB; ADD67526.

XX New hematological malignancy-related genes and polypeptides, useful for
PT screening anti-cancer agents, and generating antibodies or
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT lymphocytic leukemia.

XX Claim 9; SEQ ID NO 4; 307pp; English.

XX The present invention describes an isolated polynucleotide (I), which is
CC overexpressed in haematological malignancies, and which encodes a
CC polypeptide or an immunogenic fragment of the polypeptide. Also
CC described: (1) an isolated polypeptide; (2) an expression vector
CC comprising (I) operably linked to an expression control sequence; (3) a
CC host cell comprising an expression vector; (4) an isolated antibody that
CC specifically binds to the polypeptide or its immunogenic fragment; and
CC (5) immunoconjugates comprising the antibody above, or an antibody that
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC by (I). (I) has cytostatic and immunostimulant activities, and can be
CC used in vaccines and immunotherapy. The immunoconjugates are useful in
CC the manufacture of a medicament, particularly as active ingredients in a
CC composition for treating cancer, e.g. multiple myeloma cell, chronic
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC The polynucleotide (I) or polypeptide can be used for screening anti-
CC cancer agents, and generating antibodies or immunoconjugates for treating
CC or preventing the above-mentioned diseases. The polynucleotide,
CC polypeptide or antibody can be used for detecting, diagnosing or
CC prognosticating the haematological malignancies described above. The
CC present sequence is used in the exemplification of the present invention.

XX Sequence 184 AA;

Human; transmembrane activator and intracellular CAML interactor; TAC1;
cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX Homo sapiens.
 XX WO200187979-A2.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001WO-US015567.
 XX 12-MAY-2000; 2000US-0204039P.
 XX 27-JUN-2000; 2000US-0214591P.
 XX 14-MAY-2001; 2001US-00214591.
 XX (AMGE-) AMGEN INC.
 XX Theill LE, Yu G;
 XX WPI; 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX Disclosure; Fig 10B; 94pp; English.
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein
 XX Sequence 283 AA;
 SQ Query Match 100.0%; Score 201; DB 5; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
 DB 5 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 38
 RESULT 24
 ID ABG95060 standard; protein; 288 AA.
 XX ABG95060;
 XX 04-DEC-2002 (first entry)
 DT Human translocation (4; 16)(q26; p13) protein.
 DE Chromosome aberration; oncogenic fusion protein; cancer;
 KW

KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX Homo sapiens.
 XX WO200269900-A2.
 XX 12-SEP-2002.
 XX 01-MAR-2002; 2002WO-US006518.
 XX 01-MAR-2001; 2001US-0272751P.
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 XX Fritz LC, Burrows FJ;
 XX WPI; 2002-698710/75.
 XX N-PSDB; ABS73235.
 XX Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX Disclosure; Page 189-190; 389pp; English.
 XX The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p33), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents a protein encoded by the DNA sequence of a
 CC chromosome aberration
 XX Sequence 288 AA;
 SQ Query Match 100.0%; Score 201; DB 5; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
 DB 112 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 145
 RESULT 25
 ID AAB60699 standard; protein; 302 AA.
 XX AAB60699;
 XX 11-SEP-2003 (revised)
 DT 22-MAY-2001 (first entry)
 XX

DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
 XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX WO200112812-A2.
 XX 22-FEB-2001.
 XX 16-AUG-2000; 2000WO-US022507.
 XX 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-0183536P.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 FI Thompson J;
 FI WPI; 2001-202866/20.
 DR N-PSDB; AAF59999.
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 FT lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 FT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX Example 4; Fig 2; 59pp; English.
 XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
 CC BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX Sequence 302 AA;

Query Match 100.0%; Score 201; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2,1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 34
 Db 31 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 64
 RESULT 26
 AAEE0507
 ID AAEE0507 standard; protein; 302 AA.
 XX AC AAEE0507;
 XX 11-SEP-2003 (revised)
 DT 31-JUL-2001 (first entry)
 XX Human BCMA-Immunoglobulin G Fc region fusion construct.
 XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
 KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
 KW immunoglobulin G; IgG; Fc region.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT Protein 1..22 /label= Signal peptide
 FT /note= "Derived from murine Ig kappa sequence"
 FT Protein 23..302
 FT /label= Mature_human_BCMA_IgG_Fc_fusion_protein
 FT Region 23..75 /note= "Derived from human BCMA protein"
 FT Domain 24..302 /label= Cysteine rich domain
 FT /note= "Derived from human BCMA"
 FT Region 76..302 /note= "Derived from human IgG Fc region"
 FT WO200124811-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000WO-US027579.
 XX 06-OCT-1999; 99US-0157933P.
 PR 11-FEB-2000; 2000US-0181807P.
 PR 30-JUN-2000; 2000US-0215688P.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 WPI; 2001-266242/27.
 DR N-PSDB; AAD03847.
 XX Treating a mammal for a condition associated with undesired cell
 FT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 PT antagonist.
 XX Example 1; Fig 3B; 85pp; English.
 XX The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or carcinoma.
 CC The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCM or BCMA) antagonist that antagonises the

CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is a fusion construct containing human APRIL-R also referred as BCMA or
 CC BCW protein, FC region of human immunoglobulin G (IgG) and a signal
 CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
 CC standardise OS field)

XX SQ Sequence 302 AA;
 Query Match 100.0%; Score 201; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
 |||||
 DB 31 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 64

RESULT 27
 ADG43717
 ID ADG43717 standard; protein; 302 AA.
 AC
 AC ADG43717;
 XX
 XX 26-FEB-2004 (first entry)
 XX
 XX Human B-cell maturation antigen-Fc SEQ ID NO:3.
 XX human; neurodegenerative immunological disorder; demyelination;
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
 KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
 KW gene therapy; mouse.

XX Chimeric.
 OS Homo sapiens.
 OS Mus sp.
 XX
 XX FH Key Location/Qualifiers
 FT Region 1..23
 FT /note= "Murine IgGkappa signal sequence"
 FT Region 24..74
 FT /note= "Human BCMA extracellular domain"
 FT Region 75..302
 FT /note= "Human Ig heavy chain FC region"
 XX
 XX W02003072713-A2.
 XX
 XX PD 04-SEP-2003.
 XX
 XX 21-FEB-2003; 2003WO-US005147.
 XX
 XX PR 21-FEB-2002; 2002US-0358427P.
 XX
 XX PA (BIOJ) BIOGEN INC.
 XX
 XX PI Kalled SL, Reid H;
 XX
 XX KW WPI; 2003-721758/68.
 DR N-PSDB; ADG43718.
 XX
 XX PT Treating a neurodegenerative immunological disorder, e.g. demyelination
 PT or inflammation in a mammal comprises administering a B-cell maturation
 PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

PS Claim 12; Page 70-71; 72pp; English.
 XX
 CC The invention relates to a novel method for treating a neurodegenerative
 CC immunological disorder, demyelination or Central Nervous System (CNS)
 CC inflammation in a mammal. The method comprises administering B-cell
 CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
 CC (the mammal has or is at risk of developing multiple sclerosis). The
 CC method of the invention has neuroprotective, nontropic, and
 CC antiinflammatory activity, and may have a use in gene therapy. The
 CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
 CC immunological disorder such as multiple sclerosis, demyelination or CNS
 CC inflammation. The present sequence is used in the exemplification of the
 CC invention.

XX SQ Sequence 302 AA;

Query Match 100.0%; Score 201; DB 7; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
 |||||
 DB 31 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 64

RESULT 28
 AAB60700
 ID AAB60700 standard; protein; 157 AA.

XX
 XX AAB60700;
 AC
 AC 22-MAY-2001 (first entry)
 DT
 XX
 XX Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
 XX
 XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

XX Homo sapiens.
 OS
 XX W0200112812-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 16-AUG-2000; 2000WO-US022507.
 PF
 XX 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-0183536P.

XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 PA
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 XX
 XX WPI; 2001-202866/20.
 DR N-PSDB; AAF60000.
 DR

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX
 XX Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known

as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents a human BAFF-R protein sequence as encoded by plasmid PUST535. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AAB60698

XX Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 4; Length 157;
Best Local Similarity 90.6%; Pred. No. 2.1e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
|||||
DB 7 QNEYFDSLHACIPQCLRCSSNTPLTCQRYC 35
|||||

RESULT 29
ADIS3060
ID ADIS3060 standard; peptide; 26 AA.
XX
AC ADIS3060;
XX
DT 22-APR-2004 (first entry)
XX
DE Human BCMA receptor binding site.
XX
KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; dermatological; antiasthmatic; neutrokin-alpha;
KW crystallography; cancer; allergic disorder; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW systemic lupus erythematosus; asthma; receptor.
XX
OS Homo sapiens.
XX
PN WO2003050134-A2.
XX
PD 19-JUN-2003.
XX
PF 07-NOV-2002; 2002WO-US035661.
XX
PR 07-NOV-2001; 2001US-0331049P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Oren DE, Arnold E, Volovik Y;
XX
DR WPI; 2003-532895/50.
XX
PT New crystalline Neutrokin-alpha protein, useful for designing compounds that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the activity of a Neutrokin-alpha protein for treating e.g. cancer or allergic disorders.
XX

PS Disclosure; Fig 4; 362pp; English.
XX
CC The invention relates to a neutrokin-alpha protein in crystalline form.
CC The crystalline neutrokin-alpha protein is useful for designing
CC molecules that have biological activity or compounds that bind, inhibit or mimic a neutrokin-alpha protein and/or enhance the activity of a neutrokin-alpha protein. The three-dimensional structure of a neutrokin-alpha protein is useful in determining the three-dimensional of other neutrokin-alpha proteins and their homologs. The compounds that mimic, prevent or inhibit the activity of the protein are useful for treating cancer, allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the residues in the CC receptor for binding a cytokine ligand.
XX

SQ Sequence 26 AA;

Query Match 75.1%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYFDSLHACIPQCLRCSSNTPLTC 30
|||||
DB 1 EYFDSLHACIPQCLRCSSNTPLTC 26
|||||

RESULT 30
AAB08844
ID AAB08844 standard; peptide; 185 AA.
XX
AC AAB08844;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of murine BCMA polypeptide.
XX
KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
OS Mus musculus.

XX Key Location/Qualifiers
FT Domain 47..72
FT /note= "putative transmembrane domain"

XX WO2000050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US004925.

XX 24-FEB-1999; 99US-0121485P.

XX (GEO) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene expression.

XX Claim 32; Fig 7B; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing

XX SQ Sequence 185 AA;

Query Match 67.7%; Score 136; DB 3; Length 185;
 Best Local Similarity 70.6%; Pred. No. 2.5e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSNTPLTCQRYC 34
 | : ||||| ||||| ||||| : |||||
 Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 31

AAAY71980
 ID AAY71980 standard; protein; 185 AA.

XX AC AAY71980;

XX AC AAY71980;

XX AC AAY71980 (first entry)

XX DE Murine B cell maturation factor (BCMA) protein.

XX KW Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa.

XX OS Mus musculus.

XX PN WO200068378-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US012266.

XX PR 06-MAY-1999; 99US-0132892P.

XX PR 01-MAY-2000; 2000US-0201012P.

XX PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX PI Shu HS;

XX DR WPI; 2001-016094/02.

XX DR N-PSDB; AAD02130.

XX PT Isolated TALL-1 protein is used to identify compounds that regulate B

XX PT lymphocyte proliferation, used to treat B lymphocyte associated

XX PT autoimmune disorders.

XX PS Claim 37; Page 107-108; 112pp; English.

XX CC The present invention relates to Tumour necrosis factor (TNF) and Apol-
 CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte

CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a murine B cell maturation factor (BCMA). BCMA is
 CC the receptor for TALL-1 protein

XX SQ Sequence 185 AA;

Query Match 67.7%; Score 136; DB 4; Length 185;
 Best Local Similarity 70.6%; Pred. No. 2.5e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSNTPLTCQRYC 34
 | : ||||| ||||| ||||| : |||||
 Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 32

AAE15490

ID AAE15490 standard; protein; 185 AA.

XX AC AAE15490;

XX AC AAE15490;

XX DT 12-MAR-2002 (first entry)

XX DE Mouse B cell maturation (BCMA) protein.

XX KW Mouse; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Mus sp.

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US015567.

XX PR 12-MAY-2000; 2000US-0204039P.

XX PR 27-JUN-2000; 2000US-0214591P.

XX PR 14-MAY-2001; 2001US-00214591.

XX PA (AMGB-) AMGEN INC.

XX PI Theill LE, Yu G;

XX DR WPI; 2002-066686/09.

XX PT Inhibiting activity of B cell maturation protein and/or transmembrane
 XX PT activator and intracellular cyclophilin ligand interactor, by
 XX PT administering a binding partner for APRIL, a tumour necrosis factor family
 XX PT ligand.

XX PS Disclosure; Fig 11; 94pp; English.

XX CC The invention relates to a method for inhibiting TAC1 (transmembrane
 XX CC activator and intracellular CAML interactor) and/or B cell maturation
 XX CC protein (BCMA) activity in a mammal. The method comprises administering a
 XX CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 XX CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 XX CC BCMA extracellular consensus sequence, but not the extracellular region
 XX CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 XX CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

Disclosure; Fig 10B; 94pp; English.

The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a

XX New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.
XX
XX Disclosure; Page 26; 236pp; English.
PS
XX
XX The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC

CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
 CC lymphoma. The composition may also be used in treating inflammations
 CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
 CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
 CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
 CC and vasculitis. Disorders may be treated with the novel composition using
 CC gene therapy. This sequence represents a TALL-1 related protein of the
 CC invention

SQ Sequence 42 AA;

Query Match 61.7%; Score 124; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEFDLSLHACIPQLRC 21
 AAE15491
 |||||
 DB 22 CSQNEFDLSLHACIPQLRC 42

RESULT 35
 AAE15491
 ID AAE15491 standard; protein; 117 AA.

XX AAE15491;

XX
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)

DE Human-murine B cell maturation protein (BCMA) consensus sequence.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.

OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Disclosure; Fig 11; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/

CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-murine B cell maturation protein (BCMA) consensus sequence.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 117 AA;

Query Match 46.5%; Score 93.5; DB 5; Length 117;
 Best Local Similarity 69.7%; Pred. No. 0.00042;
 Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

OY 2 SONEYFDSLHACIPQLRCSSNTPPLTCORYC 34
 : |||||
 DB 2 AQCEYFDSLHAC-PC-LRCS-----PPTCQ-YC 27

RESULT 36

AAE15492

ID AAE15492 standard; peptide; 24 AA.

XX AAE15492;

XX 29-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX Human-murine BCMA consensus sequence cysteine rich region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.

XX Homo sapiens.

OS Mus sp.

OS Chimeric.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane

PT activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.

XX Disclosure; Fig 11; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-murine B cell maturation protein (BCMA) consensus sequence
 CC cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 CC Sequence 24 AA;

Query Match 45.0%; Score 90.5; DB 5; Length 24;
 Best Local Similarity 73.3%; Pred. No. 0.0002;
 Matches 22; Conservative 0; Mismatches 1; Indels 7; Gaps 4;

Qy 5 EYFDSLHACIPCOLRCSNTPTTCQRYC 34
 |||||
 Db 2 EYFDSLHAC-PC-LRCS-PPPTCQ-YC 24

RESULT 37

RAY94006.
 ID RAY94006 standard; protein; 249 AA.

AC RAY94006;

XX 20-OCT-2000 (first entry)

XX A murine znf4, a tumour necrosis factor ligand.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 XX znf4 activity; antibody production; autoimmune disease; amyloidosis;
 XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 XX immune response; immunosuppression; graft rejection; joint pain;
 XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
 XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 XX renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Mus musculus.

XX WO200040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58566.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,

PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX
 PS Disclosure; Page 163; 175pp; English.

XX The present sequence represents murine znf4, a tumour necrosis factor
 CC ligand. The extracellular domains of BR43x2 (an isoform of the
 CC transmembrane activator and CAML-interactor (TACI) receptor), TACI or
 CC BCMA (a related B cell protein) contain a cysteine rich domain, and are
 CC used for inhibiting znf4 activity. They may also be used for inhibiting
 CC BR43x2, TACI or BCMA receptor-ligand engagement associated with activated
 CC or resting B lymphocytes, effector T-cells, or with antibody production.
 CC The antibody production is associated with an autoimmune disease selected
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 CC and rheumatoid arthritis. The znf4 activity and BR43x2, TACI or BCMA
 CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli

XX Sequence 249 AA;

Query Match 35.6%; Score 71.5; DB 3; Length 249;
 Best Local Similarity 35.3%; Pred. No. 0.57;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 1 CSONEVFDLLHACIPCOLRCSNTPTTCQRYC 34
 |||||

Db 6 CPKQDWDSRKSVCSCALTCQSRS-QRTCTDFC 38

RESULT 38

ADCT71568

ID ADCT71568 standard; protein; 1548 AA.

XX AC ADCT71568;

XX 18-DEC-2003 (first entry)

XX Mouse subtilisin-like protein convertase 6 (SPC6).

XX neuroleptic; subtilisin-like protein convertase 6 agonist;
 KW subtilisin-like protein convertase 6 antagonist; transgenic;
 KW subtilisin-like protein convertase 6; SPC6; schizophrénia.

XX Mus sp.

XX US2003093824-A1.

XX 15-MAY-2003.

XX 25-JUN-2002; 2002US-00180903.

XX 26-JUN-2001; 2001US-0300978P.

XX 24-SEP-2001; 2001US-0324820P.

XX (ALLE/) ALLEN K D.

XX Allen KD;

XX WPI; 2003-777261/73.

XX N-PSDB; ADCT71567.

XX New transgenic mouse useful in methods for identifying potential
 PT therapeutic agents for treating a variety of diseases, including
 PT schizophrénia, comprises a disruption in a subtilisin-like protein
 PT convertase 6 (SPC6) gene.

XX Disclosure; SEQ ID NO 2; 34pp; English.

XX The invention describes a transgenic mouse (I) comprising a disruption in

CC a subtilisin-like protein convertase (SPC6) gene, where there is no

CC native expression of an endogenous SPC6 gene. The therapeutic agent is

CC administered by inhalation or insufflation or oral, buccal, parenteral,

CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,

CC intraocular, intraarterial, or rectal route. The transgenic mouse and

CC associated methods are useful for identifying potential therapeutic

CC agents (e.g. SPC6 agonists and antagonists) for treating conditions

CC associated with SPC6. The identified agents are potentially useful for

CC treating diseases such as schizophrenia. The mouse is useful for

CC investigating the biological roles of SPC6. This is the amino acid

CC sequence of mouse SPC6.

XX SQ Sequence 1548 AA;

Query Match 33.6%; Score 67.5; DB 7; Length 1548;

Best Local Similarity 37.8%; Pred. No. 12;

Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPP-----LTCQR 32

DB 1152 CAAVEYWDGSHRCQPHKCKRCGSPGSDQCYTCPR 1188

RESULT 39

ABB80243

ID ABB80243 standard; protein; 1877 AA.

AC ABB80243;

XX 04-DEC-2003 (first entry)

DE Murine subtilase.

XX Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;

KW renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;

KW pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;

KW proteinase convertase subtilisin; furin-like repeat; Alzheimer's disease;

KW Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;

KW gastritis; ulcers; urinary incontinence; lupus nephritis;

KW renal transplant rejection; myocardial infarction; erectile dysfunction;

KW ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;

KW congestive heart failure; ischaemia; hypertensive vascular disease.

XX Mus musculus.

XX WO2003060109-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-EP0000253.

XX 15-JAN-2002; 2002US-0347876P.

XX 29-JUL-2002; 2002US-0398734P.

XX (FARB) BAYER AG.

XX Koehler RH;

XX WPI; 2003-608065/57.

XX New subtilase-encoding polynucleotide and its encoded protein, useful for

PT identifying modulators of subtilase activity, and in gene therapy for

PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or

PT ischemia.

XX Disclosure; Page 122-26; 135pp; English.

XX This sequence shows a murine subtilase. The homologous human subtilase

CC coding sequence is located on chromosome 9q21.13. Related EST's are

expressed in kidney (renal cell adenocarcinoma), head and neck tissue,

heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,

uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin

protein is a long membrane bound protein which shows 96% identity to

human proprotein convertase subtilisin. There are two blocks of 11 furin-

like repeats in the C-terminal portion of the protein. It has one

transmembrane domain, also in the C-terminal portion, suggesting that the

protein is localised on the outside of the membrane. The subtilase

polynucleotide and polypeptide are useful for identifying test compounds,

which may act as agonists or antagonists at the receptor site and which

can be regulated to provide therapeutic effects. Vectors comprising the

polynucleotide are useful for modulating the activity of subtilase in a

disease, e.g. a central nervous system disorder, a gastrointestinal

disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or

diabetes. In particular, these diseases are Alzheimer's disease,

Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,

gastritis, ulcers, urinary incontinence, lupus nephritis, renal

transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,

lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,

congestive heart failure, myocardial infarction, ischaemia, hypertensive

vascular diseases, etc. These are also useful for preventing or

ameliorating the diseases cited above

XX SQ Sequence 1877 AA;

Query Match 33.6%; Score 67.5; DB 7; Length 1877;

Best Local Similarity 37.8%; Pred. No. 14;

Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPP-----LTCQR 32

DB 1481 CAAVEYWDGSHRCQPHKCKRCGSPGSDQCYTCPR 1517

RESULT 40

AAE15495

ID AAE15495 standard; peptide; 33 AA.

AC AAE15495;

XX 12-MAR-2002 (first entry)

XX Human TACI cysteine-rich consensus region #1.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;

KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;

KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;

KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;

KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane

PT activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Claim 1; Fig 12B; 94pp; English.

PS The invention relates to a method for inhibiting TACI (transmembrane
 XX activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, proctitis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 XX is human TACI cysteine-rich consensus region

SQ Sequence 33 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 33;

Best Local Similarity 32.4%; Pred. No. 0.32;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDLLHACIPCOLRCSSNTPLTCQRYC 34

Db 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAFC 33

RESULT 41

ADA49368

ID ADA49368 standard; peptide; 33 AA.

AC ADA49368;

XX 20-NOV-2003 (first entry)

XX Human TACI1 cysteine rich domain.

XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
 KW antiarthritic; dermatological; antidiabetic; neuroprotective;
 KW antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
 KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
 KW pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; TACI1; CRD;
 KW cysteine rich domain.

XX Homo sapiens.

XX WO2003035846-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348922P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.

XX Disclosure; Page 617; 618pp; English.

PS The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting abgr; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antithyroidic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases: rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents a cysteine rich
 CC domain (CRD) module of human TACI1.

XX Sequence 33 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 33;

Best Local Similarity 32.4%; Pred. No. 0.32;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDLLHACIPCOLRCSSNTPLTCQRYC 34

Db 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAFC 33

RESULT 42

AAU10951

ID AAU10951 standard; protein; 37 AA.

XX AAU10951;

XX 12-MAR-2002 (first entry)

XX Human AGP-3 receptor cysteine rich repeat region #1.

XX Human; AGP-3; antiinflammatory; antithyroidic; immunosuppressive;
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.

XX WO200185782-A2.

XX 15-NOV-2001.

XX 12-FEB-2001; 2001WO-US004568.

XX 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Hsu H;

PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.
 XX
 PS Disclosure; Fig 8; 153pp; English.

CC The present sequence represents an alternatively spliced human TACI
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
 CC for preparing a composition for treating systemic lupus erythematosus

XX Sequence 266 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 266;

Best Local Similarity 32.4%; Pred. No. 2.7; Mismatches 1; Gaps 1;

Matches 11; Conservative 8; Indels 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

Db 34 CPBEQYWDPLGLTGMSCCKTICNHQS-QRTCAAF 66

RESULT 49

AAU10949

ID AAU10949 standard; protein; 291 AA.

XX

AC AAU10949;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human AGP-3 receptor extracellular domain.

XX

Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 dermatological; neuroprotective; nontropic; immunomodulator; metabolic;
 antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.

OS

WO200185782-A2.

XX

PD 15-NOV-2001.

XX

PF 12-FEB-2001; 2001WO-US004568.

XX

PR 11-FEB-2000; 2000US-0181800P.

XX

FA (AMGE-) AMGEN INC.

XX

PI Boyle WJ, Hsu H;

XX

DR WPI; 2002-049441/06.

XX

FT Composition, useful for identifying modulator of receptor for treating
 FT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor
 FT ligand family member) receptor and encoding nucleic acids.

XX

PS Claim 1; Fig 18; 124pp; English.

XX

CC The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vesicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds (agonists
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful

CC for identifying intracellular proteins that interact with the respective
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
 CC involved in B cell growth, survival and activation particularly in lymph
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
 CC identified using (II) are used for modulating B cell response and are
 CC used to treat diseases characterised by inflammatory processes or
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the
 CC production of hybridoma cells, which are derived from B cells, which
 CC involves treating the hybridoma cells with (II). (II) is useful in the
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,
 CC septic shock, etc. The nucleic acids are also useful for developing the
 CC transgenic animals expressing (II), which are useful for producing the
 CC polypeptides and for the study of in vivo biological activity. The
 CC present sequence represents the amino acid sequence of human AGP-3
 CC extracellular domain

XX Sequence 291 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 291;

Best Local Similarity 32.4%; Pred. No. 2.9;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

Db 34 CPBEQYWDPLGLTGMSCCKTICNHQS-QRTCAAF 66

RESULT 50

AAW75783

ID AAW75783 standard; protein; 293 AA.

XX

AC AAW75783;

XX

DT 18-JAN-1999 (first entry)

XX

DE Human lymphocyte surface receptor TACI.

XX

TACI; transmembrane activator and CAML-interactor;

calcium signal-modulating cyclophilin ligand; human;

lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;

cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;

immunosuppressive; graft versus host disease; transplant rejection;

XX therapy.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Domain

FT 1..166

FT /label= Extracellular_domain

FT /note= "Claim 8"

FT Peptide

FT 34..71

FT /note= "TNFR_NGFR motif"

FT Domain

FT 167..186

FT /label= Transmembrane_domain

FT Domain

FT 187..294

FT /label= Cytoplasmic_domain

FT /note= "Claim 6"

XX

XX WO9839361-A1.

XX

PD 11-SEP-1998.

XX

PF 03-MAR-1998; 98WO-US004270.

XX

PR 03-MAR-1997; 97US-00810572.

XX

(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

PI Bram RJ, Von Bulow G;

DR WPI; 1998-506346/43.

DR N-PSDB; AAV57328.

New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.

PS Claim 20; Fig 2a; 89pp; English.

This is the amino acid sequence of novel human transmembrane activator and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targeted to specifically regulate B cell responses without affecting T cell activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also claimed are the C-terminal (see AAW5784) and N-terminal (see AAW5785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI protein. Methods are claimed for identifying a ligand for TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting mature T lymphocytes. TACI can be activated to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating autoimmune and inflammatory conditions such as immune complex- induced vasculitis, glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II collagen-induced arthritis, experimental allergic and hyperacute xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus, transplant rejection, cancer or graft versus host disease

SQ Sequence 293 AA;

Query Match 33.1%; Score 66.5; DB 2; Length 293;

Query Match 33.1%; SCORE 88.5; D
Best Local Similarity 32.4%; Pred. No. 2.9;

Best Local Similarity 32.4%, Freq. NO. 2.5,
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

1 CSQNEYFDSLHACIPCQLRCSSTPPLTCQRYC 34 QY

34 CP E E Q Y W D P L L G T C M S C K T I C N H Q S - Q R T C A A F C 66

Search completed: January 28, 2005, 19:52:44

Job time : 39.3395 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:37:53 ; Search time 196.661 Seconds
(without alignments)
335.635 Million cell updates/sec

Title: US-10-077-137-1
Perfect score: 964
Sequence: 1 MLQAGQCSQNEYPDSLHA.....CKSLPALSAATEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	3	AA088843 Amino aci
2	964	100.0	184	3	AA094001 A human B
3	964	100.0	184	4	AA09241 Human BCM
4	964	100.0	184	4	AA09241 Human BCM
5	964	100.0	184	4	AA09241 Human BCM
6	964	100.0	184	4	AA09241 Human BCM
7	964	100.0	184	4	AA09241 Human BCM
8	964	100.0	184	4	AA09241 Human BCM
9	964	100.0	184	4	AA09241 Human BCM
10	964	100.0	184	4	AA09241 Human BCM
11	964	100.0	184	4	AA09241 Human BCM
12	964	100.0	184	4	AA09241 Human BCM
13	964	100.0	184	4	AA09241 Human BCM
14	964	100.0	184	4	AA09241 Human BCM
15	964	100.0	184	4	AA09241 Human BCM
16	964	100.0	184	4	AA09241 Human BCM
17	964	100.0	184	4	AA09241 Human BCM
18	964	100.0	184	4	AA09241 Human BCM
19	964	100.0	184	4	AA09241 Human BCM
20	964	100.0	184	4	AA09241 Human BCM
21	964	100.0	184	4	AA09241 Human BCM
22	964	100.0	184	4	AA09241 Human BCM
23	964	100.0	184	4	AA09241 Human BCM
24	964	100.0	184	4	AA09241 Human BCM
25	964	100.0	184	4	AA09241 Human BCM

99 78.5 8.1 293 5 AAO14130 Human tra
100 78.5 8.1 293 5 ABB81488 Human TAC

ALIGNMENTS

RESULT 1
ID AAB08843 standard; peptide; 184 AA.

XX AAB08843;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of human.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Domain 57..77
XX /note= "putative transmembrane domain"

XX WO2000050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US004925.

XX 24-FEB-1999; 99US-0121485P.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression.

XX Claim 32; Fig 7A; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX a necrosis factor (NF)-kB activator. The method of the invention is used
XX to identify compounds which modulate BCMA activity (and thus NF-kB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the reporter
XX gene is altered as a result of contact with library. The method is useful
XX for identifying polypeptides which increase or decrease gene expression
XX from a promoter. The BCMA polypeptide or nucleic acid are useful for
XX preparing a pharmaceutical composition for treating cancer, apoptosis,
XX viral infections, inflammatory response, such as rheumatoid arthritis,
XX inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-kB expression and thus for drug
XX designing

XX Sequence 184 AA;

XX Query Match 100.0%; Score 964; DB 3; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-95;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQSQNEYFDSLLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKGTHAILWTCL 60

Db 1 MLQWAGQSQNEYFDSLLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKGTHAILWTCL 60
Qy 61 GLSLIIISLAVFLVLMFLLRKISSBPLKDFKNTGSLGGLGMANIDLEKSGRTGDEIILPRGLE 120
Db 61 GLSLIIISLAVFLVLMFLLRKISSBPLKDFKNTGSLGGLGMANIDLEKSGRTGDEIILPRGLE 120
Qy 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
Db 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 2

AAAY94001

ID AAY94001 standard; protein; 184 AA.

XX AC AAY94001;

XX DT 20-OCT-2000 (first entry)

XX A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX znf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO2000040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58559.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used
XX with activated or resting B lymphocytes, effector T-cells, or with
XX antibody production. The antibody production is associated with an
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,

CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. B843x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Qy 61 GLSLIIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTGDDEIILPRGLE 120
 Db 61 GLSLIIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTGDDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 3
 AAE09241
 ID AAE09241 standard; protein; 184 AA.

XX AC AAE09241;
 XX 19-NOV-2001 (first entry)
 XX Human BCMA protein.
 XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 OS Homo sapiens.
 XX W0200160397-A1.
 XX 23-AUG-2001:
 XX 28-NOV-2000; 2000WO-US032378.
 XX 16-FEB-2000; 2000US-0182938P.
 PR 22-AUG-2000; 2000US-0226986P.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;
 XX WPI; 2001-541628/60.
 DR N-PSDB; AAD15902.
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.
 XX Example 2; Fig 2; 160pp; English.
 PS The invention relates to methods of using one or more agonists or
 XX

CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human BCMA protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Qy 61 GLSLIIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTGDDEIILPRGLE 120
 Db 61 GLSLIIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTGDDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 4
 AAY71979
 ID AAY71979 standard; protein; 184 AA.

XX AC AAY71979;
 XX 28-MAR-2001 (first entry)
 XX Human B cell maturation factor (BCMA) protein.
 DE Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and ApOL-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Domain 1..62
 FT /label= Extracellular_domain
 FT
 XX W0200068378-A1.
 XX 16-NOV-2000.
 XX 05-MAY-2000; 2000WO-US012266.
 XX 06-MAY-1999; 99US-0132892P.
 PR 01-MAY-2000; 2000US-0201012P.
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX Shu HS;
 XX WPI; 2001-016094/02.
 DR

DR N-PSDB; AAD02125.

XX Isolated TALL-1 protein is used to identify compounds that regulate B

PT lymphocyte proliferation, used to treat B lymphocyte associated

PT autoimmune disorders.

XX Claim 37; Page 104-105; 112pp; English.

PS The present invention relates to Tumour necrosis factor (TNF) and Apol-

CC related Leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules,

CC proteins (including homologues), and their antibodies. The invention in

CC particular relates to methods for regulating the interaction between TALL

CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to

CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.

CC TALL-1 protein is useful for identifying compounds that regulate B

CC lymphocyte proliferation. It is also useful for treating B lymphocyte

CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus

CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple

CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,

CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal

CC glomerulonephritis, or polyarthritis nodosa. The TALL-1 protein and its

CC corresponding nucleic acid sequence are also useful in diagnostic assays.

CC The present sequence is a human B cell maturation factor (BCMA) protein.

CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome

CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not

CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.

CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression

CC increases with B lymphocyte maturation

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 9.7e-95;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKGKTNAIWTCL 60

Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKGKTNAIWTCL 60

Qy 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSLGLGMANIDLEKSGTDEIILPGL 120

Db 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSLGLGMANIDLEKSGTDEIILPGL 120

Qy 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Db 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184

Db 181 ISAR 184

RESULT 5

AAB60698

ID AAB60698 standard; protein; 184 AA.

XX

AC AAB60698;

XX

DT 22-MAY-2001 (first entry)

XX

DE Human BAFF receptor (BAFF-R).

XX

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

KW immune-related disorder; B-cell growth inhibitor; BCMA;

KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

KW renal disorder; immunosuppressive disorder; HIV infection;

KW organ transplantation; antiinflammatory; systemic lupus erythematosus;

KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;

KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;

KW lymphoma; gene therapy; cancer; tumour.

XX

OS Homo sapiens.

XX WO200112812-A2.

XX 22-FEB-2001.

PD

XX 16-AUG-2000; 2000WO-US022507.

PF

XX 17-AUG-1999; 99US-0149378P.

PR

XX 11-FEB-2000; 2000US-0181684P.

PR

XX 18-FEB-2000; 2000US-0183536P.

XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTECH R & D SA.

XX

PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

PI Thompson J;

XX WPI; 2001-202866/20.

DR N-PSDB; AAF59998.

XX

PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell

PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,

PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.

XX

XX Claim 20; Fig 1; 59pp; English.

PS The invention relates to the use of a BAFF receptor (BAFF-R, also known

CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the

CC treatment of a variety of immune-related disorders. BAFF-R is a member of

CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory

CC agent, and also plays a role in the development of hypertension and

CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-

CC specific antibodies can be used for inhibiting B-cell growth, dendritic

CC cell-induced B-cell growth and maturation, and immunoglobulin production,

CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative

CC disorders, hypertension and renal disorders. The BAFF-R proteins may also

CC be used in the treatment of immunosuppressive disorders and HIV

CC infection, and in patients undergoing organ transplantation. The BAFF-R

CC proteins or BAFF-R specific antibodies may be used for treating,

CC suppressing or altering an immune response involving a signalling pathway

CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R

CC inhibits B-cell growth and maturation it is useful for treating diseases

CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,

CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly

CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding

CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,

CC autoimmune disorders and inherited B-cell-associated disorders. The

CC present sequence represents human BAFF-R

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 9.7e-95;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKGKTNAIWTCL 60

Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKGKTNAIWTCL 60

Qy 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSLGLGMANIDLEKSGTDEIILPGL 120

Db 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSLGLGMANIDLEKSGTDEIILPGL 120

Qy 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Db 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184

Db 181 ISAR 184

RESULT 6
AAE00506
ID AAE00506 standard; protein; 184 AA.
XX
AC AAE00506;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human B cell maturation protein (BCMA).
XX
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX
OS Homo sapiens.
XX
PN WO200124811-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027579.
XX
PR 06-OCT-1999; 99US-0157933P.
PR 11-FEB-2000; 2000US-0181807P.
PR 30-JUN-2000; 2000US-0215688P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX
PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
DR WPI; 2001-266242/27.
DR N-PSDB; AAD03844.
XX
XX
PT Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
PT antagonist.
XX
PS Claim 3; Fig 3A; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and human
XX immunodeficiency virus (HIV), and for treating, suppressing or altering
XX an immune response involving a signalling pathway between APRIL-R and its
XX ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
XX is human APRIL-R also referred as BCMA or BCM protein
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLQWAGQCSNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60
Db 1 MLQWAGQCSNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFLVLMFLLRKISSEPLKDEFFKNTSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFLVLMFLLRKISSEPLKDEFFKNTSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Qy 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184
RESULT 7
ABB81487
ID ABB81487 standard; protein; 184 AA.
XX
AC ABB81487;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human BCMA receptor related protein SEQ ID NO:7.
XX
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO200238766-A2.
XX
PD 16-MAY-2002.
XX
PP 05-NOV-2001; 2001WO-US047018.
XX
PR 07-NOV-2000; 2000US-0246449P.
PR 20-DEC-2000; 2000US-0257131P.
PR 28-JUN-2001; 2001US-0301715P.
PR 29-AUG-2001; 2001US-0315565P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gross JA, Xu W, Henne RM, Grant FJ;
XX
DR WPI; 2002-508212/54.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
PS Disclosure; Page 135-136; 154pp; English.
XX
CC The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid

CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGDEIILPRGLE 120
DB 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
DB 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
DB 181 ISAR 184

RESULT 8
ABP54694
ID ABP54694 standard; protein; 184 AA.
XX
AC ABP54694;
XX
DT 30-DEC-2002 (first entry)
XX
DE Metastatic colorectal cancer-associated polypeptide.
XX
KW Colorectal cancer; metastasis; differential expression; cytostatic;
KW diagnosis; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
FN WO200268677-A2.
XX
PD 06-SEP-2002.
XX
PF 27-FEB-2002; 2002WO-US006001.
XX
PR 27-FEB-2001; 2001US-0272206P.
PR 02-APR-2001; 2001US-0281149P.
PR 17-APR-2001; 2001US-0284555P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
FI Mack DH, Markowitz SD;
XX
DR WPI; 2002-698677/75.
DR N-PSDB; ABQ81560.
XX
PT New genes that are up- or down-regulated in colorectal cancer, useful for
PT diagnosing colorectal cancer in a subject, or for identifying modulators
PT of colorectal cancer-associated proteins and genes for treating
PT colorectal cancer.
XX
PS Claim 8; Page 255; 260pp; English.
XX

CC The present sequence is the protein sequence of a human polypeptide
CC encoded by a gene that exhibits decreased expression in colon cancer-
CC derived metastases compared to normal colon tissue. It is an example of
CC claimed polypeptides that are encoded by genes which are differentially
CC expressed in metastatic colorectal cancer cells. Such polypeptides are
CC useful in diagnostic and prognostic assays, for raising antibodies useful
CC e.g. in immunotherapy, and in screening for modulator compounds of
CC therapeutic value
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGDEIILPRGLE 120
DB 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
DB 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
DB 181 ISAR 184

RESULT 9
AAE28961
ID AAE28961 standard; protein; 184 AA.
XX
AC AAE28961;
XX
DT 27-JAN-2003 (first entry)
XX
DE Human B-cell maturation antigen (BCMA).
XX
KW Human; tumour; B-cell maturation antigen; transmembrane activator;
KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
KW BCMA; multiple myeloma.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Region 1..54
FT Domain /note= "Antigenic epitope"
FT /note= "Extracellular domain"
FT Region 8..41
FT /note= "Cysteine rich region"
XX
PN WO200266516-A2.
XX
PD 29-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003500.
XX
PR 20-FEB-2001; 2001US-0270274P.
PR 12-APR-2001; 2001US-0283447P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Kindsvogel W;
XX
DR WPI; 2002-723183/78.
DR N-PSDB; AAD46410.

XX B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.
 XX
 XX Disclosure; Page 63; 67pp; English.
 PS
 CC The invention relates to the manufacture of a composition for inhibiting
 CC the proliferation of tumour cells. The method involves using an antibody
 CC component that binds both the B-cell maturation antigen (BCMA) and the
 CC transmembrane activator and calcium-modulator and cyclophilin ligand-
 CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
 CC for inhibiting proliferation of tumour cells, particularly inhibiting
 CC ZTNF4 activity in a mammal associated with increased endogenous antibody
 CC production or a disorder consisting of neoplasm, chronic lymphocytic
 CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
 CC lymphoproliferative disease or light chain gammopathy or inflammation
 CC e.g. asthma. The invention is also useful in gene therapy. The present is
 CC human BCMA protein
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTSNKGKTNAILWTCL 60
 Db 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTSNKGKTNAILWTCL 60
 Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSKPKVDSHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSKPKVDSHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184
 RESULT 10
 AAE35216
 ID AAE35216 standard; protein; 184 AA.
 XX
 AC AAE35216;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Human B-cell maturation receptor (BCMA) protein.
 XX
 KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW B-cell maturation receptor; BCMA; receptor.
 XX
 OS Homo sapiens.
 XX
 XX WO200294852-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 20-MAY-2002; 2002WO-US015910.
 XX
 XX 24-MAY-2001; 2001US-0293343P.
 XX
 XX (ZTMO) ZYMOGENETICS INC.

XX Rixon MW, Gross JA;
 XX WPI; 2003-148455/14.
 DR N-PSDB; AAD53754.
 XX
 PT Transmembrane activator and calcium modulator and cyclophilin ligand-
 PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
 PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
 XX
 PS Disclosure; Col 100; 71pp; English.
 XX
 CC The invention relates to fusion proteins comprising transmembrane
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an
 CC immunoglobulin. The invention is used to manufacture a medicament for
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The
 CC composition comprising the fusion protein may also be used in treating
 CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
 CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
 CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
 CC rejection, anaemia and septic shock. The fusion proteins are also used in
 CC gene therapy. The present sequence is human B-cell maturation receptor
 CC (BCMA) protein used in the invention
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTSNKGKTNAILWTCL 60
 Db 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTSNKGKTNAILWTCL 60
 Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSKPKVDSHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSKPKVDSHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184
 RESULT 11
 ADA49361
 ID ADA49361 standard; protein; 184 AA.
 XX
 AC ADA49361;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human BCMA protein.
 XX
 KW human; TALL-1; antagonist; immunosuppressive; antirheumatic;
 KW antiinflammatory; antiarthritic; dermatological; antidiabetic;
 KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
 KW vaccine; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
 KW multiple sclerosis; myasthenia gravis; Grave's disease;
 KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
 KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA.
 XX
 OS Homo sapiens.
 XX
 XX WO2003035846-A2.
 XX
 XX

PD 01-MAY-2003.
 XX 24-OCT-2002; 2002WO-US034376.
 PF 24-OCT-2001; 2001US-0345106P.
 PR 14-JAN-2002; 2002US-0348962P.
 PR 07-FEB-2002; 2002US-0354966P.
 PR 13-AUG-2002; 2002US-0403364P.
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX Zhang G, Shu H, Liu Y, Xu L;
 PI WPI; 2003-403345/38.
 XX N-PSDB; ADA49360.
 DR Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
 XX activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.
 XX Claim 62; Page 613; 618pp; English.
 PS The invention relates to a novel TALL-1 antagonist protein, comprising a
 XX sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting abgr; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipruritic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
 QY 61 GLSLIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 DB 61 GLSLIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 QY 121 YTVECTCEDCICKPKVDSHCHPFLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
 DB 121 YTVECTCEDCICKPKVDSHCHPFLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 12
 ID ABP60552
 AC ABP60552 standard; protein; 184 AA.
 XX
 XX ABP60552;
 XX
 XX 28-MAR-2003 (first entry)
 DT Human tumour necrosis factor BCMA.
 XX
 XX

KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
 KW antithyroid; cytostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculosic; antidiabetic;
 KW antipeptidic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.
 OS Homo sapiens.
 XX WO200294192-A2.
 XX 28-NOV-2002.
 XX 22-MAY-2002; 2002WO-US016106.
 XX 24-MAY-2001; 2001US-0293100P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM;
 PI WPI; 2003-156740/15.
 DR Novel isolated antibody that immunospecifically binds tumour necrosis
 XX factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.
 PT Disclosure; Page 222; 225pp; English.
 XX The invention relates to a novel antibody or its fragment, which
 PS immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 CC antiallergic, antidiabetic, neuroprotective, ophthalmological,
 CC tuberculosic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor BCMA
 XX Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
 QY 61 GLSLIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 DB 61 GLSLIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 QY 121 YTVECTCEDCICKPKVDSHCHPFLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
 DB 121 YTVECTCEDCICKPKVDSHCHPFLPAMEGATILVTTKTNDYCKSLPALSALETEIKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

Db 121 YTVECTCEDCIKSPKVDSDHCPPLPAMEBEGATILVTTKTNDYCKSLPALSALETEIEKS 180
Qy 181 ISAR 184
181 ISAR 184
Db 181 ISAR 184

RESULT 13
ID ABP97717 standard; protein; 184 AA.
XX AC ABP97717;
XX 28-MAY-2003 (first entry)
XX DE Amino acid sequence of human BCMA receptor.
XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX TALL-1; April; systemic lupus erythematosus; BCMA.
XX OS Homo sapiens.
XX PN WO2003014294-A2.
XX PD 20-FEB-2003.
XX PF 24-JUL-2002; 2002WO-US023487.
XX PR 03-AUG-2001; 2001US-0310114P.
XX PR 30-APR-2002; 2002US-037717P.
XX PA (GETH) GENENTECH INC.
XX PI Dixit V, Grewal I, Ridgway J, Yan M;
XX WPI; 2003-256560/25.
XX DR N-PSDB; ABZ68871.
XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
XX preparing a composition for treating systemic lupus erythematosus.
XX PS Disclosure; Fig 2; 153pp; English.
XX CC The present sequence represents a human BCMA polypeptide. The
XX specification also describes TACI and BR3 polypeptides. TACI and BR3 are
XX receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
XX bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
XX BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
XX preparing a composition for treating systemic lupus erythematosus
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLOWAGCQSONEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLOWAGCQSONEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120

Qy 121 YTVECTCEDCIKSPKVDSDHCPPLPAMEBEGATILVTTKTNDYCKSLPALSALETEIEKS 180
Db 121 YTVECTCEDCIKSPKVDSDHCPPLPAMEBEGATILVTTKTNDYCKSLPALSALETEIEKS 180

Qy 181 ISAR 184
181 ISAR 184
Db 181 ISAR 184

RESULT 14
ADD67527 standard; protein; 184 AA.
XX AC ADD67527;
XX 15-JAN-2004 (first entry)
XX DE Human Ly1732P protein SEQ ID NO:4.
XX KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
XX KW vaccine; immunotherapy; cancer; multiple myeloma cell;
XX KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
XX KW human.
XX OS Homo sapiens.
XX PN WO2003062401-A2..
XX PD 31-JUL-2003.
XX PF 22-JAN-2003; 2003WO-US002353.
XX PR 22-JAN-2002; 2002US-00057475.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
XX PI Carter L, Mcneill PD;
XX WPI; 2003-598749/56.
XX DR N-PSDB; ADD67526.
XX PT New hematological malignancy-related genes and polypeptides, useful for
XX screening anti-cancer agents, and generating antibodies or
XX immunoconjugates for treating e.g. multiple myeloma cell or chronic
XX lymphocytic leukemia.
XX PS Claim 9; SEQ ID NO 4; 307pp; English.
XX CC The present invention describes an isolated polynucleotide (I), which is
XX overexpressed in haematological malignancies, and which encodes a
XX polypeptide or an immunogenic fragment of the polypeptide. Also
XX described: (1) an isolated polypeptide; (2) an expression vector
XX comprising (I) operably linked to an expression control sequence; (3) a
XX host cell comprising an expression vector; (4) an isolated antibody that
XX specifically binds to the polypeptide or its immunogenic fragment; and
XX (5) immunoconjugates comprising the antibody above, or an antibody that
XX specifically binds to a polypeptide, or its immunogenic fragment, encoded
XX by (I). (I) has cytostatic and immunostimulant activities, and can be
XX used in vaccines and immunotherapy. The immunoconjugates are useful in
XX the manufacture of a medicament, particularly as active ingredients in a
XX lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
XX primates, goats, bovines, equines, porcines, lupines, canines or felines.
XX The polynucleotide (I) or polypeptide can be used for screening anti-
XX cancer agents, and generating antibodies or immunoconjugates for treating
XX or preventing the above-mentioned diseases. The polynucleotide,
XX polypeptide or antibody can be used for detecting, diagnosing or
XX prognosticating the haematological malignancies described above. The
XX present sequence is used in the exemplification of the present invention.
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLOWAGCQSONEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLOWAGCQSONEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
QY 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
Db 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 15
ADG43715
ID ADG43715 standard; protein; 184 AA.
XX
AC ADG43715;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human B-cell maturation antigen SEQ ID NO:1.
XX
KW human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003072713-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005147.
XX
PR 21-FEB-2002; 2002US-0358427P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Kalled SL, Reid H;
XX
DR WPI; 2003-721758/68.
DR N-PSDB; ADG43716.
XX
PT Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
PS Claim 8; Page 68-69; 72pp; English.
XX
CC The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nontropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence represents human BCMA.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQRCSSNTPLTCORYCNASVTNSVKGNTNAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQRCSSNTPLTCORYCNASVTNSVKGNTNAILWTCL 60
QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
QY 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
Db 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 16
ADK00756
ID ADK00756 standard; protein; 184 AA.
XX
AC ADK00756;
XX
DT 06-MAY-2004 (first entry)
XX
DE Native human BCMA.
XX
KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
KW Antibacterial; antiparasitic; systemic lupus erythematosus;
KW diabetes mellitus; AIDS; BCMA.
XX
OS Homo sapiens.
XX
PN WO2004011611-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023421.
XX
PR 25-JUL-2002; 2002US-0398530P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chuntharapai A, Grewal I, Kim KJ, Yan M;
XX
DR WPI; 2004-143841/14.
DR N-PSDB; ADK00755.
XX
PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and
PT treating pathological conditions associated with tumor necrosis factor,
PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; SEQ ID NO 6; 110pp; English.
XX
CC The present invention relates to an isolated monoclonal antibody which
CC binds to a transmembrane activator of and CAML interactor (TACI)
CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
CC polypeptide biological activity in mammalian cells, or for diagnosing and
CC treating pathological conditions associated with TNF and TNF receptor-
CC related molecules, e.g. cancer or immune-related disease, such as
CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
CC systemic vasculitis, diabetes mellitus, Crohn's disease,
CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
CC infectious diseases including AIDS, hepatitis infection, bacterial
CC infection, fungal infection, protozoal infection and parasitic infection.
CC The present sequence represents native human BCMA.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQRCSSNTPLTCORYCNASVTNSVKGNTNAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQRCSSNTPLTCORYCNASVTNSVKGNTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPGL 120
 Db 61 GLSLIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPGL 120
 Qy 121 YTVVECTCEDCIKSKPKVSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVECTCEDCIKSKPKVSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 17
 ABR40082
 ID ABR40082 standard; protein; 184 AA.
 XX
 AC ABR40082;
 XX
 DT 27-JUN-2003 (first entry)
 DE Human Genoxit.
 KW Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
 KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
 KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
 KW Type III transmembrane protein; insulin resistance; atherosclerosis;
 KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
 KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..54
 FT /label= Extracellular_domain
 FT Misc-difference 3
 FT /label= Gln, Lys
 FT Domain 55..77
 FT /label= Transmembrane_domain
 FT Domain 78..184
 FT /label= Intracellular_domain
 XX
 FN WO2003013582-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 05-AUG-2002; 2002WO-IB003498.
 XX
 PR 06-AUG-2001; 2001US-0310754P.
 XX
 PA (GEST) GENSET SA.
 XX
 PI Lucas J, Dyalynas D, Briggs K;
 XX
 DR WPI; 2003-268160/26.
 DR N-PSDB; ACC00340.
 XX
 PT New use of agonist or antagonist of Genoxit activity for preventing or
 PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
 PT atherosclerosis.
 XX
 PS Disclosure; Page 32; 35pp; English.
 XX
 CC The present invention relates to the use of an agonist or antagonist of
 CC Genoxit activity for preventing or treating obesity. Genoxit is a member
 CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
 CC transmembrane protein. The agonists or antagonists of the invention are
 CC useful for treating or preventing obesity-related diseases or disorders,
 CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
 CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
 CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
 CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic

CC complications, e.g. microangiopathic lesions, ocular lesions,
 CC retinopathy, neuropathy and renal lesions
 XX
 SQ Sequence 184 AA;
 Query Match 99.4%; Score 958; DB 6; Length 184;
 Best Local Similarity 99.5%; Pred. No. 4.3e-94;
 Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTNAILWTCL 60
 Db 1 MLXWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTNAILWTCL 60
 Qy 61 GLSLIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPGL 120
 Db 61 GLSLIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPGL 120
 Qy 121 YTVVECTCEDCIKSKPKVSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVECTCEDCIKSKPKVSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 18
 ABG95060
 ID ABG95060 standard; protein; 288 AA.
 XX
 AC ABG95060;
 XX
 DT 04-DEC-2002 (first entry)
 DE Human translocation (4; 16)(q26; p13) protein.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 FN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US006518.
 XX
 PR 01-MAR-2001; 2001US-0272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Fritz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 DR N-PSDB; ABS73235.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX
 PS Disclosure; Page 189-190; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein

CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents a protein encoded by the DNA sequence of a
 CC chromosome aberration

XX SQ Sequence 288 AA;

Query Match 99.1%; Score 955; DB 5; Length 288;
 Best Local Similarity 99.5%; Pred. No. 1.6e-93;
 Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LQAGQCSQNEYFDSLLHACIPQQLRCSNTPPLTCQRYCNASVTNSVKGNTNAILWTCLG 61
 Db 106 LQAGQCSQNEYFDSLLHACIPQQLRCSNTPPLTCQRYCNASVTNSVKGNTNAILWTCLG 165
 Qy 62 LSLIISLAVFVLMFLRLKISSEPLKDFPKNTGSGLLGMANIDLEKSRDGEIILPRGLE 121
 Db 166 LSLIISLAVFVLMFLRLKISSEPLKDFPKNTGSGLLGMANIDLEKSRDGEIILPRGLE 225
 Qy 122 TVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSI 181
 Db 226 TVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSI 285
 Qy 182 SAR 184
 Db 286 SAR 288

RESULT 19
 AAE15484
 ID AAE15484 standard; protein; 181 AA.

XX AC AAE15484;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 5..38

XX FT /note= "Cysteine-rich consensus region; This is region is
 specifically claimed as SEQ ID NO: 7 in claim 1 of the
 specification"

XX FT 52..72

XX FT /label= Transmembrane_domain

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

XX XX

PF 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane

XX activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.

XX Disclosure; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane

CC activator and intracellular CAML interactor) and/or B cell maturation

CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF

CC family ligand), having the consensus region of TACI, BCMA, or the TACI/

CC BCMA extracellular consensus sequence, but not the extracellular region

CC of TACI or BCMA. The method is useful for inhibiting activity of TACI

CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,

CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI

CC antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic

CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

CC disease), drug and insect sting allergy, inflammatory bowel disease

CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,

CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer

CC with leucocyte infiltration of the skin or organs. The present sequence

CC is human BCMA protein

XX Sequence 181 AA;

XX Query Match 98.5%; Score 950; DB 5; Length 181;

XX Best Local Similarity 100.0%; Pred. No. 3e-93;

XX Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLLHACIPQQLRCSNTPPLTCQRYCNASVTNSVKGNTNAILWTCLG 63

Db 1 MAGQCSQNEYFDSLLHACIPQQLRCSNTPPLTCQRYCNASVTNSVKGNTNAILWTCLG 60

Qy 64 LIISLAVFVLMFLRLKISSEPLKDFPKNTGSGLLGMANIDLEKSRDGEIILPRGLE 123

Db 61 LIISLAVFVLMFLRLKISSEPLKDFPKNTGSGLLGMANIDLEKSRDGEIILPRGLE 120

Qy 124 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSI 183

Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSI 180

Qy 184 R 184

Db 181 R 181

XX RESULT 20

XX AAB60700

ID AAB60700 standard; protein; 157 AA.

XX AC AAB60700;

XX 22-MAY-2001 (first entry)

DT Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

immune-related disorder; B-cell growth inhibitor; BCMA;
 B-cell maturation inhibitor; immunoglobulin production inhibitor;
 autoimmunity disorder; B-cell lymphoproliferative disorder; hypertension;
 renal disorder; immunosuppressive disorder; HIV infection;
 organ transplantation; anti-inflammation; systemic lupus erythematosus;
 autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 lymphoma; gene therapy; cancer; tumour; plasmid pUST535.
 Homo sapiens.
 W0200112812-A2.
 22-FEB-2001.
 16-AUG-2000; 2000WO-US022507.
 17-AUG-1999; 99US-0149378P.
 11-FEB-2000; 2000US-0181684P.
 18-FEB-2000; 2000US-0183536P.
 (BIOJ) BIOGEN INC.
 (APOT-) APOTEC R & D SA.
 Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 Thompson J;
 WPI; 2001-202866/20.
 N-PSDB; AAF60000.
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 Example 1; Fig 3; 59pp; English.
 The invention relates to the use of a BAFF receptor (BAFF-R, also known
 as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 treatment of a variety of immune-related disorders. BAFF-R is a member of
 the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 agent, and also plays a role in the development of hypertension and
 related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 specific antibodies can be used for inhibiting B-cell growth, dendritic
 cell-induced B-cell growth and maturation, and immunoglobulin production,
 and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 disorders, hypertension and renal disorders. The BAFF-R proteins may also
 be used in the treatment of immunosuppressive disorders and HIV
 infection, and in patients undergoing organ transplantation. The BAFF-R
 proteins or BAFF-R specific antibodies may be used for treating,
 suppressing or altering an immune response involving a signalling pathway
 between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 inhibits B-cell growth and maturation it is useful for treating diseases
 such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 autoimmune disorders and inherited B-cell-associated disorders. The
 present sequence represents a human BAFF-R protein sequence as encoded by
 plasmid pUST535. However, this BAFF-R protein sequence is 27 amino acids
 shorter than that given in AAB60698
 Sequence 157 AA;
 Query Match 74.6%; Score 719.5; DB 4; Length 157;
 Best Local Similarity 85.3%; Pred. No. 1.2e-68;
 Matches 157; Conservative 0; Mismatches 0; Indels 27; Gaps 9;
 1 MLOWAGCQNEFYDLSLHACIPQLRCSNTPPLTCORYCNASVTN--GTNAILWTCL 60
 1 MLOWAGCQNEFYDLSLHACIPQLRCSNTPPLTCORYCNASVTN--GTNAILWTCL 51
 61 GLSLIIISLAVFLMFLRKISSEPLKXK---NTGSGLLGMANIDLEKSGRTGDEILPRGLE 120
 121 YTVBECTCEDCIKSKPKVSDHCFPPAPMEGATILVTTNTNDYCKSLPALSALETEKS 180
 103 YTVBECT---CIKSKPKVSDHCFPLP---EGATILVTTNTNDYCKS---ALSATEIEKS 153
 181 ISAR 184
 154 ISAR 157
 Db 52 GLSLIIIS---FVLMFLRLKISSEPLKXK---NTGSGLLGMANIDLEKSGRTGDEILPRGLE 102
 Qy 121 YTVBECTCEDCIKSKPKVSDHCFPPAPMEGATILVTTNTNDYCKSLPALSALETEKS 180
 Db 103 YTVBECT---CIKSKPKVSDHCFPLP---EGATILVTTNTNDYCKS---ALSATEIEKS 153
 Qy 181 ISAR 184
 Db 154 ISAR 157
 RESULT 21
 AAB08844
 ID AAB08844 standard; peptide; 185 AA.
 XX AAB08844;
 AC AC
 DT 02-JAN-2001 (first entry)
 XX Amino acid sequence of murine BCMA polypeptide.
 DE BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX Mus musculus.
 OS XX
 FH Key Location/Qualifiers
 FT Domain 47..72
 FT /note= "putative transmembrane domain"
 XX W0200050633-A1.
 XX 31-AUG-2000.
 PD 24-FEB-2000; 2000WO-US004925.
 PP 24-FEB-1999; 99US-0121485P.
 PR (GEHO) GEN HOSPITAL CORP.
 PA Seed B, Ting A;
 PI WPI; 2000-558405/51.
 XX Identifying a modulator of gene expression for drug designing, by
 contacting a compound library with a cell expressing an anti-cell death
 gene and reporter gene, and determining alteration in reporter gene
 expression.
 PT Claim 32; Fig 7B; 53pp; English.
 XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
 a necrosis factor (NF)-kB activator. The method of the invention is used
 to identify compounds which modulate BCMA activity (and thus NF-kB
 activity). The specification describes a method of identifying a
 polypeptide which increases gene expression from a promoter. The method
 involves contacting a library of with a cell which expresses a
 recombinant anti-cell death gene and a reporter gene operably linked to
 the promoter, and then determining whether the expression of the reporter
 gene is altered as a result of contact with library. The method is useful
 for identifying polypeptides which increase or decrease gene expression
 from a promoter. The BCMA polypeptide or nucleic acid are useful for
 preparing a pharmaceutical composition for treating cancer, apoptosis,
 viral infections, inflammatory response, such as rheumatoid arthritis,
 inflammatory bowel disease or septic shock. BCMA is useful for
 identifying compounds that modulate NF-kB expression and thus for drug
 designing
 XX Sequence 185 AA;
 SQ Query Match 59.3%; Score 572; DB 3; Length 185;
 Best Local Similarity 62.6%; Pred. No. 9.6e-53;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;	
Qy	4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTNAIILWTCIGLS 63
Db	1 MAQCQFSEYFDSLHACKPCHLRCSN--PRATCQPYCDPSVTSSVKGTYTIVLWIFLGLT 58
Qy	64 LIISLAVFVLMFLRKISSEPLKDEPFN---TGSGLLGMANIDLEKSRGTGDEIILPRGL 119
Db	59 LVLSLALFTISFLLRKMNPEALKDEPQSPQLDGSQAQLDKADTELTRIRAGDDRIFFPSRL 118
Qy	120 EYTVVECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db	119 EYTVVECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Qy	178 EKSISAR 184
Db	179 EKPTHTR 185
RESULT 22	
AAAY71980	
ID	AAAY71980 standard; protein; 185 AA.
XX	
AC	AAAY71980;
DT	28-MAR-2001 (first entry)
DE	Murine B cell maturation factor (BCMA) protein.
XX	
KW	Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW	Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
KW	therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW	systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW	thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW	haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;
KW	B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
KW	post-streptococcal glomerulonephritis; polyarteritis nodosa.
XX	
OS	Mus musculus.
XX	
PN	WO2000068378-A1.
XX	
PD	16-NOV-2000.
XX	
PF	05-MAY-2000; 2000WO-US012266.
XX	
PR	06-MAY-1999; 99US-0132892P.
XX	
PR	01-MAY-2000; 2000US-0201012P.
XX	
PA	(NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX	
PI	Shu HS;
XX	
DR	WPI; 2001-016094/02.
XX	
DR	N-PSDB; AAD02130.
XX	
PT	Isolated TALL-1 protein is used to identify compounds that regulate B
PT	lymphocyte proliferation, used to treat B lymphocyte associated
PT	autoimmune disorders.
XX	
PS	Claim 37; Page 107-108; 112pp; English.
XX	
CC	The present invention relates to Tumour necrosis factor (TNF) and Apol-
CC	related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
CC	proteins (including homologues), and their antibodies. The invention in
CC	particular relates to methods for regulating the interaction between TALL
CC	-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC	regulate monocyte, macrophage and B lymphocyte mediated immune responses.
CC	TALL-1 protein is useful for identifying compounds that regulate B
CC	lymphocyte proliferation. It is also useful for treating B lymphocyte
CC	associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC	erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC	sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC	
anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,	
pemphigus vulgaris, acute rheumatic fever, post-streptococcal	
glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its	
corresponding nucleic acid sequence are also useful in diagnostic assays.	
The present sequence is a murine B cell maturation factor (BCMA). BCMA is	
the receptor for TALL-1 protein	
XX	
SQ	Sequence 185 AA;
Query Match 59.3%; Score 572; DB 4; Length 185;	
Best Local Similarity 62.6%; Pred. No. 9.6e-53;	
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;	
Qy	4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTNAIILWTCIGLS 63
Db	1 MAQCQFSEYFDSLHACKPCHLRCSN--PRATCQPYCDPSVTSSVKGTYTIVLWIFLGLT 58
Qy	64 LIISLAVFVLMFLRKISSEPLKDEPFN---TGSGLLGMANIDLEKSRGTGDEIILPRGL 119
Db	59 LVLSLALFTISFLLRKMNPEALKDEPQSPQLDGSQAQLDKADTELTRIRAGDDRIFFPSRL 118
Qy	120 EYTVVECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db	119 EYTVVECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Qy	178 EKSISAR 184
Db	179 EKPTHTR 185
RESULT 23	
AAAE15490	
ID	AAE15490 standard; protein; 185 AA.
XX	
AC	AAE15490;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Mouse B cell maturation (BCMA) protein.
XX	
KW	Mouse; transmembrane activator and intracellular CAML interactor; TACT;
KW	cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX	rheumatoid arthritis; atherosclerosis.
OS	Mus sp.
XX	
PN	WO200187979-A2.
XX	
PD	22-NOV-2001.
XX	
PF	14-MAY-2001; 2001WO-US015567.
XX	
PR	12-MAY-2000; 2000US-0204039P.
XX	
PR	27-JUN-2000; 2000US-0214591P.
XX	
PR	14-MAY-2001; 2001US-00214591.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Theill LE, Yu G;
XX	
DR	WPI; 2002-066686/09.
XX	
PT	Inhibiting activity of B cell maturation protein and/or transmembrane
PT	activator and intracellular cyclophilin ligand interactor, by
PT	administering a binding partner for APRIL, a tumor necrosis factor family
PT	ligand.
XX	
PS	Disclosure; Fig 11; 94pp; English.

XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein
 XX Sequence 185 AA;
 SQ
 Query Match 59.3%; Score 572; DB 5; Length 185;
 Best Local Similarity 62.6%; Pred. No. 9.6e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
 QY 4 MAGQCSNEYFDSLLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCLGLS 63
 DB 1 MAQCQFSEYFDSLLHACKPCRLCSN--PPATCQPCYCDPSVTSVKGTTVTLWIFLGLT 58
 QY 64 LIISLAVFVLMFLRKISSEPLKDFKN----TGSGLLGMANIDLEKSRGTDEILPRGL 119
 DB 59 LVLSLALFTISFLRKQWNPALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFFPSL 118
 QY 120 EYTVVECTCEDCIKSKVNSDHCFLPAMEEGATILVTTKTDYCK-SLPAAL-SATEI 177
 DB 119 EYTVVECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTDYCKSVPTALQSYVMGM-178
 QY 178 EKISAR 184
 DB 179 EKPTHTR 185
 RESULT 24
 AAEL15501
 ID AAEL15501 standard; peptide; 58 AA.
 AC AAEL15501;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B cell maturation protein cysteine rich extracellular region.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001US-0214591.
 XX
 PD 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.
 XX (AMGE-) AMGEN INC.
 PA
 XX Theill LE, Yu G;
 PI
 XX WPI; 2002-066686/09.
 DR
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 FT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 PT
 XX Disclosure; Fig 13; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region
 XX
 SQ Sequence 58 AA;
 Query Match 33.5%; Score 323; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 9.9e-27;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CSQNEYPDSLLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCLGLSLI 65
 DB 1 CSQNEYPDSLLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCLGLSLI 58
 RESULT 25
 AAEL15491
 ID AAEL15491 standard; protein; 117 AA.
 AC AAEL15491;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 DE Human-murine B cell maturation protein (BCMA) consensus sequence.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX WO200187979-A2.
 XX
 PD 22-NOV-2001.


```

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFEKNYSGLLGMANIDLEKSRGTGDEIILPCGLE 120
Db 82 -----PPC-----PAPELLGGPSVFLFPPPKPKDTLMISRTPE 113
Qy 121 YTVBECTCEDCIKSPKVDSD-----HCFPLPAMEE-----GATILVTTKTNDY-- 164
Db 114 VT---CVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSYRVVSVLTVLHQDWLNL 170
Qy 165 -----CKSLPAALSGATEIEKSIS 182
Db 171 GKEYCKKVSNAKALPA-PIEKTIS 192

RESULT 27
AAE00507
ID AAE00507 standard; protein; 302 AA.
AC AAE00507;
DT 11-SEP-2003 (revised)
DT 31-JUL-2001 (first entry)
XX Human BCMA-Immunoglobulin G Fc region fusion construct.
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
KW immunoglobulin G; IgG; Fc region.
XX Homo sapiens.
OS Mus sp.;
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..22
FT /label= Signal peptide
FT /note= "Derived from murine Ig kappa sequence"
FT
FT Protein 23..302
FT /label= Mature human_BCMA-IgG_Fc_fusion_protein
FT Region 23..75
FT /note= "Derived from human BCMA protein"
FT Domain 24..302
FT /label= Cysteine rich domain
FT /note= "Derived from human BCMA"
FT Region 76..302
FT /note= "Derived from human IgG Fc region"
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027579.
XX
XX 06-OCT-1999; 99US-0157933P.
XX 11-FEB-2000; 2000US-0181807P.
XX 30-JUN-2000; 2000US-0215688P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI; 2001-266242/27.
XX N-PSDB; AAD03847.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX antagonist.

```

```

XX Example 1; Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and human
XX immunodeficiency virus (HIV), and for treating, suppressing or altering
XX an immune response involving a signalling pathway between APRIL-R and its
XX ligand. APRIL-R DNA is also useful in gene therapy. the present sequence
XX is a fusion construct containing human APRIL-R also referred as BCMA or
XX BCM protein, Fc region of human immunoglobulin G (IgG) and a signal
XX sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
XX Query Match 29.7%; Score 286.5; DB 4; Length 302;
XX Best Local Similarity 39.9%; Pred. No: 7e-22;
XX Matches 81; Conservative 13; Mismatches 54; Indels 55; Gaps 8;
Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db 24 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGVDR-THTC- 81
Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFEKNYSGLLGMANIDLEKSRGTGDEIILPCGLE 120
Db 82 -----PPC-----PAPELLGGPSVFLFPPPKPKDTLMISRTPE 113
Qy 121 YTVBECTCEDCIKSPKVDSD-----HCFPLPAMEE-----GATILVTTKTNDY-- 164
Db 114 VT---CVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSYRVVSVLTVLHQDWLNL 170
Qy 165 -----CKSLPAALSGATEIEKSIS 182
Db 171 GKEYCKKVSNAKALPA-PIEKTIS 192

RESULT 28
ADG43717
ID ADG43717 standard; protein; 302 AA.
XX
XX AC ADG43717;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Human B-cell maturation antigen-Fc SEQ ID NO:3.
XX
XX KW human; neurodegenerative immunological disorder; demyelination;
XX Central Nervous System; CNS; inflammation; B-cell maturation antigen;
XX BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
XX gene therapy; mouse.
XX OS Chimeric.
XX OS Homo sapiens.
XX OS Mus sp.
XX
XX FH Key Location/Qualifiers
XX FT Region 1..23
XX /note= "Murine IgGkappa signal sequence"
XX FT Region 24..74
XX /note= "Human BCMA extracellular domain"
XX FT Region 75..302
XX /note= "Human Ig heavy chain Fc region"

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XX WO2003072713-A2.
XX
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005147.
XX
XX 21-FEB-2002; 2002US-0358427P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Kalled SL, Reid H;
XX
XX WPI; 2003-721758/68.
XX
XX N-PSDB; ADG43718.
XX
XX
XX Treating a neurodegenerative immunological disorder, e.g. demyelination
XX or inflammation in a mammal comprises administering a B-cell maturation
XX antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
XX Claim 12; Page 70-71; 72pp; English.
XX
XX The invention relates to a novel method for treating a neurodegenerative
XX immunological disorder, demyelination or Central Nervous System (CNS)
XX inflammation in a mammal. The method comprises administering B-cell
XX maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
XX (the mammal has or is at risk of developing multiple sclerosis). The
XX method of the invention has neuroprotective, nootropic, and
XX antiinflammatory activity, and may have a use in gene therapy. The
XX methods, BCMA, and antibodies are useful for treating a neurodegenerative
XX immunological disorder such as multiple sclerosis, demyelination or CNS
XX inflammation. The present sequence is used in the exemplification of the
XX invention.
XX
XX SQ Sequence 302 AA;
XX
XX Query Match 29.7%; Score 286.5; DB 7; Length 302;
XX Best Local Similarity 39.9%; Pred. No. 7e-22;
XX Matches 81; Conservative 13; Mismatches 54; Indels 55; Gaps 8;
XX
XX 1 MLAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGNTNAILWTCL 60
XX 24 MLAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGVDK-THTC- 81
XX
XX 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
XX 82 -----PPC-----PAPELLGGPSVFLFPPKPKDTLMISRTPE 113
XX
XX 121 YTVBECTEDCIKSKPKVDS-----HCFPLPAMEE-----GATILVTTKNDY-- 164
XX 114 VT--CVVVDVSHEDPEVKFNWYDVGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
XX
XX 165 -----CKSLPALSAATEIEKSIS 182
XX 171 GKVKYKRVSNKALPA-PIEKTIS 192
XX
XX RESULT 29
XX AAE15488
XX ID AAE15488 standard; protein; 283 AA.
XX
XX AC AAE15488;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human BCMA-immunoglobulin Fc region fusion protein.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
```

```
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; fusion protein.
OS Homo sapiens.
FN WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor family
XX ligand.
XX
XX Disclosure; Fig 10B; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein-immunoglobulin Fc region fusion protein
XX
XX SQ Sequence 283 AA;
XX
XX Query Match 29.7%; Score 286; DB 5; Length 283;
XX Best Local Similarity 37.6%; Pred. No. 7.3e-22;
XX Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;
XX
XX 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGNTNAILWTCLGLS 63
XX 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGNTNA----- 51
XX
XX 64 LIISLAVFLMFLRLKISSEPLKDFKNTGSG-----LLGMANIDLEKSGRTG 110
XX 52 -----GGGGDKTHTCCPPAPELGGPSVFLFPPKPK 84
XX
XX 111 DEILPRGLETVBECTEDCIKSKPKVDS-----HCFPLPAMEE-----GATIL 156
XX 85 DTLMSIRTPEVT---CVVVDVSHEDPEVKFNWYDVGVEVHNKTKPREEQYNSTYRVVSV 141
XX
XX 157 VTTKNDY-----CKSLPALSAATEIEKSIS 182
XX 142 LTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 173
XX
XX RESULT 30
XX AAE15485
```

ID AAE15485 standard; peptide; 51 AA.
 XX AAE15485;
 XX AC
 XX DT
 XX DT 12-MAR-2002 (first entry)
 XX DE Human B-cell maturation (BCMA) protein extracellular domain.
 XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW KW rheumatoid arthritis; atherosclerosis.
 XX OS Homo sapiens.
 XX PN WO200187979-A2.
 XX PD 22-NOV-2001.
 XX PF 14-MAY-2001; 2001WO-US015567.
 XX PR 12-MAY-2000; 2000US-0204039P.
 XX PR 27-JUN-2000; 2000US-0214591P.
 XX PR 14-MAY-2001; 2001US-00214591.
 XX PA (AMGE-) AMGEN INC.
 XX PI Theill LE, Yu G;
 XX PI WPI; 2002-066686/09.
 XX DR Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX PS Claim 1; Fig 10A; 94pp; English.
 XX CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein extracellular domain
 XX SQ Sequence 51 AA;
 Query Match 29.5%; Score 284; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGNTA 54
 DB 1 MAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGNTA 51

RESULT 31
 AAE15486
 ID AAE15486 standard; peptide; 34 AA.
 XX AAE15486;
 XX AC
 XX DT
 XX DT 12-MAR-2002 (first entry)
 XX DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
 XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW KW rheumatoid arthritis; atherosclerosis.
 XX OS Homo sapiens.
 XX PN WO200187979-A2.
 XX PD 22-NOV-2001.
 XX PF 14-MAY-2001; 2001WO-US015567.
 XX PR 12-MAY-2000; 2000US-0204039P.
 XX PR 27-JUN-2000; 2000US-0214591P.
 XX PR 14-MAY-2001; 2001US-00214591.
 XX PA (AMGE-) AMGEN INC.
 XX PI Theill LE, Yu G;
 XX PI WPI; 2002-066686/09.
 XX DR Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX PS Claim 1; Fig 10A; 94pp; English.
 XX CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein cysteine-rich consensus region
 XX SQ Sequence 34 AA;
 Query Match 20.9%; Score 201; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41
 DB 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34

RESULT 32
 ID ADA49366 standard; peptide; 34 AA.
 XX
 AC ADA49366;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human BCMA cysteine rich domain.
 XX
 KW TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
 KW antiarthritic; dermatological; antidiabetic; neuroprotective;
 KW antithyroid; antipyrretic; nephrotropic; vasotropic; vaccine;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
 KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
 KW pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
 KW cysteine rich domain.
 XX
 OS Homo sapiens.
 XX
 OS WO2003035846-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 24-OCT-2002; 2002WO-US034376.
 XX
 XX 24-OCT-2001; 2001US-0345106P.
 PR 14-JAN-2002; 2002US-0348962P.
 PR 07-FEB-2002; 2002US-0354966P.
 PR 13-AUG-2002; 2002US-0403364P.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Zhang G, Shu H, Liu Y, Xu L;
 XX
 XX WPI; 2003-403345/38.
 DR
 XX
 XX Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.
 XX
 XX Disclosure; Page 616; 618pp; English.
 XX
 CC The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting E₂g₂; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyrretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents a cysteine rich
 CC domain (CRD) module of human BCMA.
 XX
 SQ Sequence 34 AA;
 Query Match 20.9%; Score 201; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
 |||||
 Db 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
 |||||
 RESULT 33
 AAE15489
 ID AAE15489 standard; protein; 281 AA.
 XX
 AC AAE15489;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse BCMA-human immunoglobulin Fc region fusion protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FN WO200187979-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX 14-MAY-2001; 2001WO-US015567.
 XX
 PR 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Theill LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX
 XX Disclosure; Fig 10B; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 281 AA;
Query Match 19.4%; Score 187; DB 5; Length 281;
Best Local Similarity 29.8%; Pred. No. 2.9e-11;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTAAILWTCIGLS 63
DB 1 MAQQCFHSEYFDSLHACKPCHLCSN--PPATCQYCPDPSVTSSVRGS----- 47
QY 64 LIISLAVFLMFLRLKISSEPLKDFKNTGSG-----LLGWNADLLEKSR 108
DB 48 -----YTGCGGDKTKTCPCPAPELGGPSVFLPPK 80
QY 109 TGDPIILPRGLYTVBECTCEDCKSPKVDSD-----HCFPLPAMEE-----GAT 154
DB 81 PKDTLMISRTPEVT---CVVDVSHEDPEVKFNVDGVEVHNAKTPREQYNSTYRVV 137
QY 155 ILVTKTNDY-----CKSLPAALSATEIEKSIS 182
DB 138 SVLTVLHQDWLNGKEYCKVKSNKALPA-PIEKTTIS 171

RESULT 34
ABJ38417
ID ABJ38417 standard; protein; 42 AA.
AC ABJ38417;
XX
XX
DT 12-JUN-2003 (first entry)
XX
DE TALL-1 related protein SEQ ID No 197.
XX
XX TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX WO200292620-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US015273.
XX
XX 11-MAY-2001; 2001US-0290196P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Min H, Hsu H;
XX
XX WPI; 2003-156719/15.
XX
XX New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.
XX
XX Disclosure; Page 26; 236pp; English.

CC The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis

CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a TALL-1 related protein of the
CC invention
XX
SQ Sequence 42 AA;
Query Match 16.4%; Score 158; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRC 28
DB 15 MLQWAGQCSQNEYFDSLHACIPQLRC 42

RESULT 35
ADI53060
ID ADI53060 standard; peptide; 26 AA.
XX
AC ADI53060;
XX
XX 22-APR-2004 (first entry)
XX
XX Human BCVA receptor binding site.
XX
XX protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; dermatological; antiasthmatic; neurokine-alpha;
KW crystallography; cancer; allergic disorder; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW systemic lupus erythematosus; asthma; receptor.
XX
XX Homo sapiens.
XX
XX WO2003050134-A2.
XX
XX 19-JUN-2003.
XX
XX 07-NOV-2002; 2002WO-US035561.
XX
XX 07-NOV-2001; 2001US-0331049P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Oren DE, Arnold E, Volovik Y;
XX WPI; 2003-532895/50.
XX
XX New crystalline Neutrokin-alpha protein, useful for designing compounds
PT that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the
PT activity of a Neutrokin-alpha protein for treating e.g. cancer or
PT allergic disorders.
XX
XX Disclosure; Fig 4; 362pp; English.

CC The invention relates to a neutrokin-alpha protein in crystalline form.
CC The crystalline neutrokin-alpha protein is useful for designing
CC molecules that have biological activity or compounds that bind, inhibit
CC or mimic a neutrokin-alpha protein and/or enhance the activity of a
CC neutrokin-alpha protein. The three-dimensional structure of a neutrokin
CC -alpha protein is useful in determining the three-dimensional of other
CC neutrokin-alpha proteins and their homologs. The compounds that mimic,
CC prevent or inhibit the activity of the protein are useful for treating
CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC erythematosus or asthma. This sequence represents the residues in the
XX receptor for binding a cytokine ligand.

XX
SQ Sequence 26 AA;
Query Match 15.7%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 12 EYFDSLLHACIPQQLRCSSTNPPLTC 37
DB 1 EYFDSLLHACIPQQLRCSSTNPPLTC 26

RESULT 36
ABB78398
ID ABB78398 standard; protein; 175 AA.
XX
AC ABB78398;
XX
DT 17-DEC-2002 (first entry)
XX
DE Amino acid sequence of murine TRAF3-binding B cell-specific receptor.
XX
KW Mouse; TRAF3-binding B cell-specific receptor; TRAF3;
KW signal transduction; TNF ligand; cancer; autoimmune disease; apoplexia;
KW viral infection; AIDS; bone disease; transplantation rejection;
KW Alzheimer's disease; ischaemia; rheumatoid arthritis; cachexia.
XX
OS Mus sp.
XX
XX WO200272827-A1.
XX
XX 19-SEP-2002.
XX
XX 28-FEB-2002; 2002WO-JP001849.
XX
XX 28-FEB-2001; 2001JP-00055119.
XX
XX (RIKE ) RIKEN KK.
XX
XX (IRIE/) IRIE S.
XX
XX (SATO/) SATO T.
XX
XX Irie S, Sato T;
XX
XX WPI; 2002-713516/77.
XX
XX N-PSDB; ABV72373.
XX
XX TRAF3-binding B cell-specific receptor and encoded gene, applicable in
XX diagnosis of abnormality due to TRAF3-mediated intracellular signal
XX transduction and in screening drugs for e.g. cancer, autoimmune diseases
XX and AIDS.
XX
XX Claim 1; Page 47-48; 57pp; Japanese.
XX
XX The present sequence represents a murine TRAF3-binding B cell-specific
XX receptor. The polynucleotide and polypeptide sequence of this receptor
XX are useful for diagnosis of abnormality due to TRAF3-mediated
XX intracellular signal transduction and in screening drugs for diseases
XX associated with TNF ligand family and TNF receptor-ligand superfamily
XX e.g. cancer, autoimmune diseases, viral infections like AIDS, bone
XX diseases, transplantation rejection, Alzheimer's disease, ischaemia,
XX rheumatoid arthritis, apoplexia and cachexia
XX
XX Sequence 175 AA;
XX
Query Match 12.1%; Score 116.5; DB 5; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.00056;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSNEVFDSLLHACIPQQL-----RCSSTNPPLTCQRYCNASVTNSVK---GTNAIL 56
DB 21 QCNQTECFDPLVRNCVSCELFHTPTDGTHTSSLEPGTALQPOEGSALRPDVALLVGAPALL 80
QY 57 WTCGLSLI--ISLAVFMFLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSTGD 111
DB 81 GLILALTGLVLSVSWRQQLRTASPDTSSEGVQOE-----SLENVFPVPSSET-- 129
QY 112 EIIIPRGLEYTVECTCEDCKIKSPKVDSCFPLPAMEGATILVTTKT 161
DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATELGSLTELVTIKT 170

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```

RESULT 37
AAE22244
ID AAE22244 standard; protein; 175 AA.
XX
AC AAE22244;
XX
DT 25-JUL-2002 (first entry)
XX
DE Murine BAFF receptor (BAFF-R) protein.
XX
XX Murine; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation;
XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX myasthenia gravis; hypertension; organ transplantation; drug screening;
XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular; TNF;
XX renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
XX haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
XX multiple myeloma; chromosomal mapping; tissue typing; drug screening.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Domain 70..97
XX /label= Transmembrane_domain
XX
XX WO200224909-A2.
XX
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US028006.
XX
XX 18-SEP-2000; 2000US-0233152P.
XX
XX 21-SEP-2000; 2000US-0234140P.
XX
XX 13-FEB-2001; 2001US-0268499P.
XX
XX 14-AUG-2001; 2001US-0312185P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
XX
XX N-PSDB; AAD35411.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for treating,
XX preventing or delaying e.g. autoimmune diseases, cancers, inherited
XX genetic disorders involving B-cells, cardiovascular disorders, or renal
XX disorders.
XX
XX Example 4; Fig 4b; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
XX Necrosis Factor (TNF) family, which is associated with the expression of
XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
XX useful for treating, preventing or delaying autoimmune diseases, cancer,
XX tumorigenic conditions or inherited genetic disorders involving B-cells,
XX hypertension, cardiovascular disorders, immunosuppressive diseases, renal
XX disorders, inflammation, organ transplantation and HIV. Autoimmune
XX diseases, which can be treated or prevented by BAFF-R, include systemic
XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
XX cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and
XX monoclonal gammopathy of undetermined significance. The nucleic acids,
XX protein, protein homologues, and antibodies may further be used in
XX screening assays, in detection assays (chromosomal mapping, tissue typing
XX or forensic biology), predictive medicine (e.g. diagnostic or prognostic
XX assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
XX are further useful as immunogens to raise anti-BAFF-R antibodies, or in
XX screening drugs or compounds that modulate BAFF-R activity or expression.

```


CC The present sequence is murine BAFF-R protein

Sequence 175 AA:

Query Match	12.1%	Score 116.5	DB 5	Length 175
Best Local Similarity	29.4%	Pred. No. 0.00056		
Matches	50	Conservative	21	Mismatches 64
				Indels 35
				Gaps 8

QY 7 QCSONEYFDSLHACIPCQL-----RCSSNTPPLTCORYCNASVTNSVK--GTNAIL 56

Db 21 QCNQTECFDPLVRNCVSCFHTPTDGTSSLEFGTALQOEGSALRPDVALLVGAPALL 80

QY 57 WTCLGLSLI--ISLAVFLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111

[illegible]

QY 112 EIILPRGLEYTVEECTCEDCIKSKPKVSDSDHCFPLPAMEEGATILVTTKT 161

```

130 -----PHASAPTWPPPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT 170
Db

```

RESULT 38

ABB81489

ID ABB81489 standard; protein; 175 AA.

AC ABB81489:

DT 02-SEP-2002 (first entry)

XX DE Mouse Ztnfr12 protein SEO ID NO:13.

Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritis; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft-rejection; Crohn's disease.

MS
M118 8D

XX PN WQ200238766-A2.

XX
PD
16-MAY-2002XX
PF 05-NOV-2001. 2001WO-IIS047018XX
BB 07-NOV-2000: 2000US-0246449B

20-DEC-2000: 2000US-0257131P.

PR 28-JUN-2001; 2001US-0301715P.

PR 29-AUG-2001; 2001US-0315565P.

PA (ZYMO) ZYMOGENETICS INC.

PI Gross JA, Xu W, Henne RM, Grant FJ;

WPI: 2002-508212/54.

DR N-PSDB: ABN89431.

Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.

PS Disclosure: Page 140: 154pp: English.

The present invention describes a human tumour necrosis factor receptor designated ztnfr12 (I). (I) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive

XX The present sequence represents a murine BR3 polypeptide. The
CC specification also describes TAC1 polypeptides. TAC1 and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 175 AA;

Query Match 12.1%; Score 116.5; DB 6; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.00056;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

Qy 7 QCSQNEYFDSLHACIPCOL-----RCSNTPLTCQRYCNASVNSVK---GTNAIL 56
Db 21 QCNTECFDPLVRNCVSGELEHTPDTHGTSLEPGTALQPGSGALPVDVALLVGAPALL 80
Qy 57 WTCIGLSLI--ISLAVFLMFLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTD 111
Db 81 GLILALTLVGLVLSVSWRWRQQLRTASPDTSQGVQOE-----SLENVFPVPSSET-- 129
Qy 112 EIILPRGLETVVECTCEDCKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
Db 130 ----PHASAPTWPLK-EDADSALPR----HSVFPVPA TELGSELVTTKT 170

RESULT 40
AAE22266
ID AAE22266 standard; protein; 185 AA.
XX
AC AAE22266;
DT 25-JUL-2002 (first entry)
XX
DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
FT Misc-difference 27 /note= "Wild type Leu substituted with Pro"
XX
FN WO200224909-A2.
XX
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US028006.
XX
XX 18-SEP-2000; 2000US-0233152P.
XX 21-SEP-2000; 2000US-0234140P.
XX 13-FEB-2001; 2001US-0268499P.
XX 14-AUG-2001; 2001US-0312185P.
XX
XX (BIOJ) BIOGEN INC.
XX Ambrose CM, Thompson JS;
XX

DR WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for treating,
PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
PT genetic disorders involving B-cells, cardiovascular disorders, or renal
PT disorders.
XX
XX Example 17; Page; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant. Note: The present
CC sequence is not shown in the specification but is derived from human BAFF
CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
CC specification
XX
SQ Sequence 185 AA;

Query Match 11.0%; Score 106.5; DB 5; Length 185;
Best Local Similarity 26.4%; Pred. No. 0.0071;
Matches 48; Conservative 23; Mismatches 62; Indels 49; Gaps 8;

Qy 8 CSQNEYPSLLHACIPCOL-----RCSNTPLTC---QRYCNASVNSVKGNAL 55
Db 19 CNETCFDPLVRHCVCGLLRTPRPKAGASSPAPRTALQPQESVGAGAGAAALPLPGL 78
Qy 56 LW---TCLGLSLIISLAVFLMF-----LLRKTSSPLKDFKNTGSGLLGMANIDLEK 106
Db 79 LFGAPALLGLALVIALVLVGLVSWRWRQQLRTASPDTSQGVQOE----- 128
Qy 107 SRTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
Db 129 ----DKVII---LSPGISDATAWPPPGEDPGTTP-----GHSVPVPATELGSELVTT 177
Qy 160 KT 161
Db 178 KT 179

RESULT 41
AAE22267
ID AAE22267 standard; protein; 185 AA.
XX
XX AAE22267;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T.
XX
XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX myasthenia gravis; hypertension; organ transplantation; drug screening;
XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular;

renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
OS Homo sapiens.
FH Key Location/Qualifiers
XX Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
FT FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
FT FT
XX WO200224909-A2.
XX 28-MAR-2002.
XX 06-SEP-2001; 2001WO-US028006.
XX 18-SEP-2000; 2000US-0233152P.
XX 21-SEP-2000; 2000US-0234140P.
XX 13-FEB-2001; 2001US-0268499P.
XX 14-AUG-2001; 2001US-0312185P.
XX (BIOJ) BIOGEN INC.
XX Ambrose CM, Thompson JS;
XX WPI; 2002-362428/39.
XX New human BAFF receptor proteins and nucleic acids, useful for treating,
PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
PT genetic disorders involving B-cells, cardiovascular disorders, or renal
PT disorders.
XX Example 17; Page; 164pp; English.
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant. Note: The present
CC sequence is not shown in the specification but is derived from human BAFF
CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
CC specification
XX SQ Sequence 185 AA;
Query Match 10.9%; Score 105.5; DB 5; Length 185;
Best Local Similarity 26.4%; Pred. No. 0.0091;
Matches 48; Conservative 23; Mismatches 62; Indels 49; Gaps 8;
QY 8 CSQNEYFDSLHACIPQCL-----RCSNTPPLTC---QRNCNASVTNSVKGTNAI 55

Db 19 CNQTECFDLLVRHCACGLRTPRPKPAGAASSPAPRTALQPOESVGAGAEALPLPGL 78
QY 56 LW---TCLGSLIISLAVFVLMF-----LLRKISSEPLKDEPKNTKSGLLGMANIDLEK 106
Db 79 LFGAPALLGLALVIALVGLVSRRRQRRLRGASSAAEPDGKDAPEPL----- 128
QY 107 SRTGDEIILPRGLEVTVECTC-----EDCIKSKPKVSDHCFPLPAMEEGATILVTT 159
Db 129 ----DKVII---LSPGISDATAPAWPPGSDPGTTP-----GHSVPVPATELGSTELVTT 177
QY 160 KT 161
Db 178 KT 179
RESULT 42
AAE15487
ID AAE15487 standard; peptide; 21 AA.
XX AC AAE15487;
XX 12-MAR-2002 (first entry)
XX Human B-cell maturation (BCMA) protein transmembrane region.
XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
XX WO200187979-A2.
XX 22-NOV-2001.
XX 14-MAY-2001; 2001WO-US015567.
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX (AMGB-) AMGEN INC.
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX Disclosure; Fig 10A; 94pp; English.
XX The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

PD 28-MAR-2002.
 XX
 XX
 XX 06-SEP-2001; 2001WO-US28006.
 XX
 XX
 XX 18-SEP-2000; 2000US-0233152P.
 PR 21-SEP-2000; 2000US-0234140P.
 PR 13-FEB-2001; 2001US-0268499P.
 PR 14-AUG-2001; 2001US-0312185P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Ambrose CM, Thompson JS;
 XX
 XX WPI; 2002-362428/39.
 XX
 XX New human BAFF receptor proteins and nucleic acids, useful for treating,
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal
 PT disorders.
 XX
 XX
 PS Example 17; Page; 164pp; English.
 XX
 XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant. Note: The present
 CC sequence is not shown in the specification but is derived from human BAFF
 CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
 CC specification
 XX
 XX SQ Sequence 185 AA;
 Query Match 10.4%; Score 100.5; DB 5; Length 185;
 Best Local Similarity 26.4%; Pred. No. 0.031;
 Matches 48; Conservative 22; Mismatches 63; Indels 49; Gaps 8;
 QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTTC---QRVCNASVTNSVKGTNAI 55
 DB 19 CVQAECDLLVRHCACGLLTPPKPAGAASSPAPRTALQPQBSVGAGAGEAALPUGL 78
 QY 56 LW----TCGLSLIISLAVFVLMF-----LIRKISSEPLKDFKNTGSGLLGHMANIDLE 106
 DB 79 LFGAPALLGLALVIALVLGLVSWRRQRRLRGASSAEAPDGDKDAPEPL-----128
 QY 107 SRTGDEILPRGLEVTVEECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159
 DB 129 ----DKVII---LSFGISDATAPAWPPPGEDGTTPP-----GHSVPVPATELGSTELVTT 177
 QY 160 KT 161
 DB 178 KT 179
 RESULT 45

ADB90663
 ID ADB90663 standard; protein; 185 AA.
 XX
 XX ADB90663;
 AC
 XX
 XX 04-DEC-2003 (first entry)
 DT
 XX
 XX TALL-1R gene.
 DE
 XX
 XX Antirheumatic; tumor necrosis factor; apoptosis; TALL-1R;
 KW rheumatoid arthritis; systemic lupus erythematosus; B cell neoplasm;
 KW multiple myeloma; immune function; Antiarthritic; Immunosuppressive;
 KW Dermatological; Antiinflammatory; Fungicide; Protozoicide; Antibacterial;
 KW Virucide; Antidiarrhetic; Antipsoriatic; Antiallergic; Antiasthmatic;
 KW Neuroprotective; Antidiabetic; Cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003024991-A2.
 PN
 XX
 XX 27-MAR-2003.
 PD
 XX
 XX 20-SEP-2002; 2002WO-US030009.
 PP
 XX
 XX 21-SEP-2001; 2001US-0324238P.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Hsu H;
 PI
 XX
 XX WPI; 2003-421121/39.
 DR
 XX
 XX N-PSDB; ADB90662.
 DR
 XX
 XX Novel tumor necrosis factor and apoptosis ligand-related leukocyte-
 PT expressed ligand 1 receptor polypeptide, useful for treating rheumatoid
 PT arthritis, systemic lupus erythematosus, B cell neoplasm, or multiple
 PT myeloma.
 PT
 XX
 XX Claim 1; Page 122; 130pp; English.
 PS
 XX
 XX The present invention relates to a tumor necrosis factor and apoptosis
 CC ligand-related leukocyte-expressed ligand 1 receptor (TALL-1R)
 CC polypeptide. The polypeptide of the invention is useful for treating,
 CC preventing, or ameliorating a medical disease, condition or disorder,
 CC preferably a TALL-1R polypeptide-related disease, where the disease
 CC condition or disorder is rheumatoid arthritis, systemic lupus
 CC erythematosus, a B cell neoplasm, multiple myeloma, or is associated with
 CC inflammation or immune function. The polypeptide is useful for diagnosing
 CC a pathological condition or a susceptibility to a pathological condition
 CC in a subject. The present sequence represents a TALL-1R gene of the
 CC invention.
 XX
 XX SQ Sequence 185 AA;
 Query Match 10.4%; Score 100; DB 7; Length 185;
 Best Local Similarity 23.8%; Pred. No. 0.035;
 Matches 44; Conservative 25; Mismatches 62; Indels 54; Gaps 8;
 QY 8 CSQNEYFDSLHACIPCOLRCSNTPPLTCQRVCNASVTNSVKGT-----52
 DB 19 CVPTCEYDILLVRKVCVCRLLRKS--PPKTA-----AGASSPAPGTALQPQBSVGTSGSEV 71
 QY 53 ----NAILW---TCGLSLIISLAVFVLMFLLRKRISSEPLKDFKNTGSGLLGHMANIDLE 105
 DB 72 SLPLPGLLFCAPALLGLVIALVILVGLV-----SWRRRQRLRGASTE-- 116
 QY 106 KSRGTGEIILPRGLEVTYV--EECTCEDCIKSKPKVDS-----HCFPLPAMEEGATIL 156
 DB 117 -APDGDKAAAPPEPLDKVILSPGTDTATAPWPPPGEDQGTTPPGHSIPVPATELGSTEL 175
 QY 157 VTTKT 161
 DB 176 VTTKT 180

CC are further useful as immunogens to raise anti-BFRR antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant. Note: The present
 CC sequence is not shown in the specification but is derived from human BAFF
 CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
 CC specification
 XX
 XX SQ Sequence 185 AA;
 Query Match 10.3%; Score 99.5; DB 5; Length 185;
 Best Local Similarity 25.8%; Pred. No. 0.04; Indels 49; Gaps 8;
 Matches 47; Conservative 23; Mismatches 63; Indels 49; Gaps 8;
 QY 8 CSQNEYDLSLHACIPCOL-----RCSSNTPLTC---QRYCNASVTNSVKGTFNAI 55
 DB 19 CNTECFDILLVRHCVACGLLRTPRPKPAGAAASPAPRTALQPQESVGAGAEALPLPGL 78
 QY 56 LW---TCIGLSLISLAVFVMP-----LKRISSEPLKDEPKNTGSGLLGMANIDLEK 106
 DB 79 LFGAPALLGLALVLLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL----- 128
 QY 107 SRTGDEIILPRGLEVTVEECTC-----EDCIKSKPKVSDHCFPLPAMEEGATILVTT 159
 DB 129 ----DKVII---LSPGISDATAPANPPPGSDPGTTPP-----GHSVPVFATELGSTELVTT 177
 QY 160 KT 161
 DB 178 KT 179
 RESULT 47
 AAE22270
 ID AAE22270 standard; protein; 185 AA.
 XX
 AC AAE22270;
 XX
 DT 25-JUL-2002 (first entry)
 DE Human BAFF receptor (BAFF-R) mutant, V20N.
 XX
 KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
 FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
 FT
 XX
 PN WO200224909-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-US028006.
 XX
 PR 18-SEP-2000; 2000US-0233152P.
 PR 21-SEP-2000; 2000US-0234140P.
 PR 13-FEB-2001; 2001US-0268499P.
 PR 14-AUG-2001; 2001US-0312185P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Ambrose CM, Thompson JS;
 DR WPI; 2002-362428/39.
 XX
 PT New human BAFF receptor proteins and nucleic acids, useful for treating,
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal
 PT disorders.
 XX
 PS Example 17; Page; 164pp; English.
 XX
 CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides

Db 19 CVPACFDLLVRHCVACGLLTPRPKPAGASSAPARTALQPSVSGAGAEALPLPGL 78
 Qy 56 LW---TCLGLSLIISLAVFLMF-----LLRKISSEPLKDEFKNTGSLGGMANIDLEK 106
 Db 79 LFGAPALLGLALVLALVLGLVSWRRORRLRGASSAEPDGDKAPEPL----- 128
 Qy 107 SRTGDEIILPRGLEVTVEECTC-----EDCIKSPKVDSDHCFPLPAMEEGATILVTT 159
 Db 129 ---DKVII---LSPGISDATAPAWPPGPDGPTTP-----GHSVPVPATELGSSTELVTT 177
 Qy 160 KT 161
 Db 178 KT 179

RESULT 49

ABB81483
 ID ABB81483 standard; protein; 184 AA.

XX AC ABB81483;

XX DT 02-SEP-2002 (first entry)

XX XX Human Ztnfr12 protein SEQ ID NO:2.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaethmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease;
 KW chromosome 22q13.2.

XX OS Homo sapiens.

XX PN WO200238766-A2.

XX XX 16-MAY-2002.

XX XX 05-NOV-2001; 2001WO-US047018.

XX XX 07-NOV-2000; 2000US-0246449P.

XX XX 20-DEC-2000; 2000US-0257131P.

XX XX 28-JUN-2001; 2001US-0301715P.

XX XX 29-AUG-2001; 2001US-0315565P.

XX XX (ZYMO) ZYMOGENETICS INC.

XX FI Gross JA, Xu W, Henne RM, Grant FJ;

XX DR WPI; 2002-508212/54.

XX DR N-PSDB; ABB89426.

XX PT Novel isolated human tumor necrosis factor receptor polypeptide, termed

XX PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage

XX PT renal failure or renal disease and lymphoma.

XX PS Claim 3; Page 133; 154pp; English.

XX CC The present sequence represents a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiaethmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating

CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel disease. (I) is useful for
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. Human Ztnfr12 is located to chromosome 22q13.2
 XX
 SQ Sequence 184 AA;

Query Match 9.6%; Score 93; DB 5; Length 184;

Best Local Similarity 26.5%; Pred. No. 0.2;
 Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSNTP--PLTCQRYCNASVTSVKGNTNAIL 56

Db 19 CVPACFDLLVRHCVACGLLTPRPKPAGASSAPARTALQPSVSGAGAEALPLPGL 78

Qy 57 W---TCLGLSLIISLAVFLMF-----LLRKISSEPLKDEFKNTGSLGGMANIDLEKS 107

Db 79 FGAPELLGLALVLALVLGLVSWRRORRLRGASSAEPDGDKAPEPL----- 127

Qy 108 RTGDEIILPRGLEVTVEECTC-----EDCIKSPKVDSDHCFPLPAMEEGATILVTTK 160

Db 128 ---DKVII---LSPGISDATAPAWPPGPDGPTTP-----GHSVPVPATELGSSTELVTTK 177

Qy 161 T 161

Db 178 T 178

RESULT 50

AAE35227

ID AAE35227 standard; protein; 184 AA.

XX AC AAE35227;

XX XX 28-MAY-2003 (first entry)

XX XX Human Ztnfr12 receptor protein.

XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW Ztnfr12; receptor.

XX OS Homo sapiens.

XX PN WO200294852-A2.

XX XX 28-NOV-2002.

XX XX 20-MAY-2002; 2002WO-US015910.

XX XX 24-MAY-2001; 2001US-0293343P.

XX XX (ZYMO) ZYMOGENETICS INC.

XX XX Rixon MW, Gross JA;

XX DR WPI; 2003-148455/14.

XX DR N-PSDB; AAD53775.

XX PT Transmembrane activator and calcium modulator and cyclophilin ligand-

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:52:54 ; Search time 30.2569 Seconds
(without alignments)
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Title: US-10-077-137-1_COPY_8_41

Perfect score: 201

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Total number of hits satisfying chosen parameters: 1608061

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	201	100.0	51	9	US-09-855-158-6
5	201	100.0	58	9	US-09-854-864-21
6	201	100.0	58	9	US-09-855-158-21
7	201	100.0	81	9	US-09-854-864-13
8	201	100.0	181	9	US-09-855-158-13
9	201	100.0	181	9	US-09-854-864-5
10	201	100.0	181	9	US-09-855-158-5
11	201	100.0	184	13	US-10-077-438-1
12	201	100.0	184	13	US-10-077-438-7
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184	100.0	201	16	14	US-10-151-882-47	Sequence 47, Appli
184	100.0	201	17	14	US-10-115-193-8	Sequence 8, Appli
184	100.0	201	18	14	US-10-115-193-8	Sequence 7, Appli
184	100.0	201	19	14	US-10-152-363A-27	Sequence 27, Appli
184	100.0	201	20	14	US-10-216-074-11	Sequence 11, Appli
184	100.0	201	21	14	US-10-087-080-39	Sequence 39, Appli
184	100.0	201	22	14	US-10-742-634-9	Sequence 9, Appli
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 89 59.5 29.6 845 10 US-09-839-446-12 Sequence 12, Appl
 90 59.5 29.6 880 14 US-10-104-047-2834 Sequence 2834, Ap
 91 59.5 29.6 897 14 US-10-239-663-35 Sequence 35, Appl
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 93 59.5 29.6 914 14 US-10-406-073-6 Sequence 6, Appl
 94 59.5 29.6 939 16 US-10-480-172-22 Sequence 22, Appl
 95 59.5 29.6 974 9 US-09-898-570-14 Sequence 14, Appl
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 98 59.5 29.6 993 14 US-10-239-663-36 Sequence 36, Appl
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 100 59.5 29.6 993 14 US-10-406-073-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
 US-09-854-864-7
 ; Sequence 7, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-864-7

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 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Sequence 7, Application US/09855158
 ; Publication No. US20020086018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
 ; TITLE OF INVENTION: 3, AND TACI
 ; FILE REFERENCE: A-686A
 ; CURRENT APPLICATION NUMBER: US/09/855,158
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
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; ORGANISM: Homo sapiens
 US-09-855-158-7
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 US-09-854-864-6
 ; Sequence 6, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
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 US-09-854-864-6

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 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
 ; TITLE OF INVENTION: 3, AND TACI
 ; FILE REFERENCE: A-686A
 ; CURRENT APPLICATION NUMBER: US/09/855,158
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: US 60/204,039
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 US-09-855-158-6

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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
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; SEQ ID NO 21
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

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RESULT 6

US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

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RESULT 7

US-09-854-864-13

; Sequence 13, Application US/09854864

; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

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Best Local Similarity 100.0%; Pred. No. 5.1e-17;
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US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
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; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

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RESULT 9

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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-5

RESULT 7

US-09-854-864-13

```

; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

```

```

Query Match      100.0%; Score 201; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
|||||
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 38
|||||

```

```

RESULT 10
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5

```

```

Query Match      100.0%; Score 201; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
|||||
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 38
|||||

```

```

RESULT 11
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT

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; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

```

```

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
|||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 41
|||||

```

```

RESULT 12
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

```

```

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
|||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 41
|||||

```

```

RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey

```

APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
US-10-077-137-1

Query Match 100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 14

US-10-077-137-7
Sequence 7, Application US/10077137
Publication No. US20020172674A1
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
US-10-077-137-7

Query Match 100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 15

US-10-068-725-2
Sequence 2, Application US/10068725
Publication No. US20030012783A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
FILE REFERENCE: 01-04
CURRENT APPLICATION NUMBER: US/10/068,725
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/270,274
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/283,447
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-068-725-2

Query Match 100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 16

US-10-151-882-47
Sequence 47, Application US/10151882
Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 47
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-882-47

Query Match 100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 17

US-10-115-192-8
Sequence 8, Application US/10115192
Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: A083PCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02

```
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 18
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 19
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27
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```
Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 20
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 21
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorect
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
```



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; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 22
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 201; DB 17; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 23
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match      100.0%; Score 201; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
```

```
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 24
US-09-855-158-9
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match      100.0%; Score 201; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 25
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match      100.0%; Score 201; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 31 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 64
```

```
RESULT 26
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          90.0%; Score 181; DB 13; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSL-----LHACIPQCLRCSSNTPTLTCLHACIPQCLRCSSNTPTLTQRYC 34
DB 46 CSQNEYFDSLHACIPQCLRCSSNTPTLTCLHACIPQCLRCSSNTPTLTQRYC 99

RESULT 27
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020175674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match          90.0%; Score 181; DB 13; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSL-----LHACIPQCLRCSSNTPTLTCLHACIPQCLRCSSNTPTLTQRYC 34
DB 46 CSQNEYFDSLHACIPQCLRCSSNTPTLTCLHACIPQCLRCSSNTPTLTQRYC 99

RESULT 28
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/Agp-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match          67.7%; Score 136; DB 9; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
DB 5 CPHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 29
US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match          67.7%; Score 136; DB 9; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
```

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 30

US-10-216-074-17
; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: SHU, HONG-BING
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match 67.7%; Score 136; DB 14; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 31

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 9; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 32

US-09-855-158-10
; Sequence 10, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match 67.7%; Score 136; DB 9; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 33

US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match 61.7%; Score 124; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRC 21

Db 22 CSQNEYFDSLHACIPQCLRC 42

RESULT 34

US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11


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/ FILE REFERENCE: PF253PI
/ CURRENT APPLICATION NUMBER: US/09/879,919
/ CURRENT FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/016,812
/ PRIOR FILING DATE: 1996-03-14

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match      33.1%; Score 66.5; DB 9; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 48
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match      33.1%; Score 66.5; DB 9; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 49
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match      33.1%; Score 66.5; DB 9; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 50
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match      33.1%; Score 66.5; DB 9; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

Search completed: January 28, 2005, 20:13:09
Job time : 32.2569 secs
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:45:08 ; Search time 40.5138 Seconds
(without alignments)
436.984 Million cell updates/sec

Title: US-10-077-137-1
Perfect score: 964
Sequence: 1 MLQWAGCQSQNEFYDSLHA.....CKSLPAALSATEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR.79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	2 S43486	B-cell maturation
2	88.5	9.2	217	2 C97344	amino acid ABC tra
3	86.5	9.0	858	2 T08891	prominin - mouse
4	83.5	8.7	1998	2 T13009	protein-tyrosine k
5	82	8.5	1009	2 A57434	protein-tyrosine k
6	81.5	8.5	2233	2 T28669	surface protein 51
7	81	8.4	773	2 D89010	protein R08F11.7 [
8	79.5	8.2	1009	2 S60248	protein-tyrosine k
9	79.5	8.2	1299	2 T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2 D64469	potassium channel
11	78	8.1	841	2 JC5894	killer cell inhibi
12	77.5	8.0	738	2 D86345	hypothetical prote
13	77.5	8.0	968	2 T01733	hypothetical prote
14	77	8.0	522	2 T45824	hypothetical prote
15	77	8.0	539	2 F72288	methyl-accepting c
16	76.5	7.9	357	2 T21152	hypothetical prote
17	76.5	7.9	1404	2 T19277	hypothetical prote
18	76	7.9	744	2 A43353	ascites siialoglyco
19	76	7.9	748	2 T47250	complex I intermed
20	75.5	7.8	638	2 T41478	probable transcrip
21	75	7.8	450	2 B97297	hydrogenase chain
22	75	7.8	857	1 A41369	S-receptor kinase
23	74.5	7.7	384	2 S45592	ERD1 protein - yea
24	74.5	7.7	1101	2 T16840	hypothetical prote
25	74	7.7	377	2 JC7535	chitinase (EC 3.2.
26	73.5	7.6	307	2 B95039	membrane protein [
27	73.5	7.6	307	2 A97967	conserved hypothet
28	73	7.6	304	2 A89882	hypothetical prote
29	73	7.6	679	2 B96599	protein F20N2.12 [

30	73	7.6	733	1	A46373	probable serine/th
31	72.5	7.5	243	2	T31144	hypothetical prote
32	72.5	7.5	408	2	B84518	hypothetical prote
33	72	7.5	416	2	S75097	hypothetical prote
34	72	7.5	855	2	T10665	hypothetical prote
35	71.5	7.4	105	2	T10350	hypothetical prote
36	71.5	7.4	627	2	B71709	hypothetical prote
37	71	7.4	227	2	F72334	conserved hypothet
38	71	7.4	414	2	G71331	probable cell divi
39	71	7.4	473	2	AF1207	ABC transporters (
40	71	7.4	480	2	G88690	protein F41H10.1 [
41	71	7.4	500	2	T10543	hypothetical prote
42	71	7.4	660	2	T02268	spike glycoprotein
43	70.5	7.3	188	2	H82933	hypothetical prote
44	70.5	7.3	412	2	T24023	hypothetical prote
45	70.5	7.3	424	2	T14525	S-locus-specific g
46	70.5	7.3	490	2	T32003	hypothetical prote
47	70.5	7.3	839	2	S54174	DNA topoisomerase
48	70.5	7.3	906	2	T01440	hypothetical prote
49	70.5	7.3	1171	2	A42916	metabotropic gluta
50	70.5	7.3	1548	2	S34583	serine proteinase
51	70.5	7.3	2718	2	A23475	G surface protein
52	70.5	7.3	2824	2	T22759	hypothetical prote
53	70	7.3	513	2	A70378	histidine kinase s
54	70	7.3	726	2	T08769	hypothetical prote
55	70	7.3	1072	2	T13156	metabotropic gluta
56	69.5	7.2	315	1	B69812	serine proteinase
57	69.5	7.2	350	2	T39795	G surface protein
58	69.5	7.2	441	2	C84667	probable ubiquitin
59	69.5	7.2	573	2	T40496	probable protein k
60	69.5	7.2	574	2	T51799	methylation enzyme
61	69.5	7.2	576	2	S26583	CuB1-like protein
62	69.5	7.2	614	2	H83978	chaperonin hsp60 -
63	69.5	7.2	768	2	S52684	GTP-binding protei
64	69.5	7.2	854	2	T14377	probable membrane
65	69.5	7.2	1180	2	JC2132	S-receptor kinase
66	69.5	7.2	1212	2	JC2131	metabotropic gluta
67	69.5	7.2	1706	2	S84499	metabotropic gluta
68	69.5	7.2	2958	2	S64921	zinc finger protei
69	69.5	7.2	5376	2	T42215	probable membrane
70	69	7.2	324	1	G1MS	zonadhesin - mouse
71	69	7.2	379	2	S46711	Ig gamma-1 chain C
72	69	7.2	393	1	G1MSM	hypothetical prote
73	69	7.2	444	2	PC4436	Ig gamma-1 chain C
74	69	7.2	446	2	F86107	monoclonal antibod
75	69	7.2	459	2	T27657	anaerobic dicarbox
76	69	7.2	502	2	T20130	hypothetical prote
77	69	7.2	694	2	T10565	hypothetical prote
78	69	7.2	704	2	T50303	hypothetical prote
79	69	7.2	838	2	T20125	hypothetical prote
80	69	7.2	2322	2	T10542	hypothetical prote
81	68.5	7.1	328	2	C81677	carbohydrate isome
82	68.5	7.1	402	2	T06629	hypothetical prote
83	68.5	7.1	409	2	S44346	RAD23 protein homo
84	68.5	7.1	575	2	S29316	chaperonin 60 - cu
85	68.5	7.1	577	2	S26582	chaperonin hsp60 -
86	68.5	7.1	653	2	G96675	hypothetical prote
87	68	7.1	198	2	B89008	protein W08A12.3 [
88	68	7.1	590	2	S17920	finger protein zfp
89	68	7.1	794	2	D84765	similar to mammali
90	68	7.1	810	2	C72785	probable aldehyde
91	68	7.1	1140	2	T41457	chromosomal protei
92	68	7.1	1203	2	B55094	genome polyprotein
93	68	7.1	3386	1	GNWVDF	beta-lactoglobulin
94	67.5	7.0	178	1	LGBO	hypothetical prote
95	67.5	7.0	241	2	H81327	conserved hypothet
96	67.5	7.0	245	2	H69471	hypothetical prote
97	67.5	7.0	268	2	A71966	hypothetical prote
98	67.5	7.0	283	2	T24998	hypothetical prote
99	67.5	7.0	336	2	H72618	hypothetical prote
100	67.5	7.0	383	2	P96582	hypothetical prote

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCMA protein; BEL protein
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43486; S31208; S36661
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A>Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LA3>
A:CROSS-references: UNIPROT:Q02223; EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:94712
R:Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,
EMBO J. 11, 3897-3904, 1992
A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA2>
A:CROSS-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:G29408
A:Accession: S36661
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-184 <LA3>
A:CROSS-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:CROSS-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Incrons: 44/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 964; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.1e-81;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLWAGQSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGTMNAILWTCL 60
Db 1 MLWAGQSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGTMNAILWTCL 60
Qy 61 GLSLIISLAVFVLMFLRKISSEPLKDEKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRKISSEPLKDEKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
Qy 121 YTVSECTCEDCIKSKPKVDSHCHFCPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVSECTCEDCIKSKPKVDSHCHFCPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 2

C97344
amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium acetobu
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97344
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: C97344
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-217 <KUR>
A:CROSS-references: UNIPROT:Q97D61; GB:AE001437; PIDN:AAK81542.1; PID:g15026719; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3619
C:Superfamily: histidine permease protein M

Query Match 9.2%; Score 88.5; DB 2; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.97;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;
Qy 16 SLHACIPQCLRCSSNTPPLTCORYCNASV-----TNSVKGTMNAIL-----LWTCGL 62
Db 4 SSLNKVIPVLDDGTRITLLTSSIIIGCIIGTIIAMFKTSSVKLVNLIGKFKYTWILRG 63
Qy 63 SLIISLAVFV--LMFLRKISSEPLKDEP-----KNTGS-----GLGMANIDLEKSR 108
Db 64 PLLQLQVYVYVYGLPFLSDKLWTMPKAAIILGLSLNSGAVIAETIRGGIILAINNGQFEASK 123
Qy 109 -----TGDEILPRGLETVVEEC-----TCEDCI-KSKPKVDSH 142
Db 124 ALGHTYGTWKRIILPQARVVIPPPCNEFIAMIKDTSLSVITMEELKKAQLLVSSSG 183
Qy 143 CFFLPAMEGA--TILVTTKTNDYCKSLPAALSATEIEKSIS 182
Db 184 DAVTPYLFAGIFYLITLTITFTGIFSK-----IEKKLS 215

RESULT 3

T08881
prominin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08881
R:Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A>Title: Prominin, a novel microvilli-specific polytopic membrane protein of the apical
A:Reference number: Z16512; MUID:98024147; PMID:9356465
A:Accession: T08881
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-858 <WEI>
A:CROSS-references: UNIPROT:O54990; EMBL:AF026269; NID:92559003; PIDN:AAB86715.1; PID:g2
A:Experimental source: kidney
C:Keywords: glycoprotein; membrane protein

Query Match 9.0%; Score 86.5; DB 2; Length 858;
Best Local Similarity 22.7%; Pred. No. 5.9;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
Qy 18 LHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGTMNAILWTCLGLSLIISLAVFVLMFL 77
Db 117 LVGCFPCMRC-----CNK-CGEMHQKQKQAPCRKCLGLSLIVICILMSLGIY 167
Qy 78 RKISSEPLKDEKNTGSLGGMANIDLEKSRGTGDEIL-----PRGLETVSECTCE----- 129
Db 168 GFVANQQTTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQVYTNKKA 218
Qy 130 -----DCIKS-----KPKVDSHCHFCPLPAMEGATILVTTK-TNDYCKSLPAAL-- 172
Db 219 FSDLGIGSVLGGRIKQDKPKV-----TPVLEIKAMATAIKQTDALQNMSSSLKS 271
Qy 173 ---SATEIEKSISA 183
Db 272 LQDAATQLTNLSS 285

RESULT 4

T13009
hypothetical protein T24C20.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T13009
R;Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, P.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Accession: T13009
A;Molecule type: DNA
A;Residues: 1-1998 <CHO>
A;Cross-references: UNIPROT:Q9STR8; EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A;Experimental source: cultivar Columbia; BAC clone T24C20
C;Genetics:
A;Gene: ATSP:T24C20.80
A;Map position: 3
A;Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2;
C;Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80

Query Match 8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 26;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;
QY 38 ORYNASVTVSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSSEPLKD-EFKN--TGS 94
Db 1089 ERYCSA--NSALGTFSM--C-----SSTGPFQDSSEFENSLGP 1122
QY 95 GLGGMANIDLEKSGRTGDEIILPRGLEYTVBECTCECIKSKP-----KYDSHCFPLPAM 149
Db 1123 SLVKLSLDM--SRUGD-----RGIHFDEGGSCNGRSSAPGLNTGNVNMDCGDL--M 1173
QY 150 EGATI 155
Db 1174 DGGATI 1179

RESULT 5
A57434
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
N;Alternate names: cell adhesion kinase-beta
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57434
R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobiooka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyr
A;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: A57434
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1009 <SAS>
A;Cross-references: UNIPROT:P70600; GB:D45854; NID:G100679; PIDN:BAA08290.1; PID:d1008
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology <KIN>
F;431-439/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 82; DB 2; Length 1009;
Best Local Similarity 26.9%; Pred. No. 18;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
QY 88 EFKNTGSGLLGMANIDLEKSR-----TGBEILPRGLEYTVBECTCECIKSKPV 138
Db 249 KFWNT---LAGFANIQETVRCBLIQGNWITVDLVIGPKGIQLTSDTKPTCLAEFKQI 305
QY 139 DSPHCFPLPAME-----EGATILVTTKTND-----YCK 166
Db 306 RSIRCLPLETQAVQLGIEGAPQSLSIKTSSLAERENMADLIDGYCR 353

RESULT 6
T28669
surface protein 51C - Parametium tetraurelia
C;Species: Parametium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28669
R;Nielsen, E.; You, Y.; Forney, J.

J. Mol. Biol. 222, 835-841, 1991
A;Title: Cysteine residue periodicity is a conserved structural feature of variable surf
A;Reference number: Z20504; MUID:92106337; PMID:1762150
A;Accession: T28669
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2233 <NIE>
A;Cross-references: UNIPROT:Q94711; EMBL:M65164; NID:G159974; PID:G159975; PIDN:AAA61740
C;Genetics:
A;Genetic code: SGC5

Query Match 8.5%; Score 81.5; DB 2; Length 2233;
Best Local Similarity 25.1%; Pred. No. 45;
Matches 43; Conservative 17; Mismatches 58; Indels 53; Gaps 10;
QY 6 GQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNA-SVTNSVKGTTNAILWTCLGLSL 64
Db 520 GSCYQKQ-----CSAASQDNTHAQCOQEXPLPACTLSNTKKG-----CIDLPL 561
QY 65 IISLAVFVLMFLLRKISSSEPLKDEFKNTGSGLLGMANIDL-----EKSRTGDEIILPRGLE 120
Db 562 TCSA-----LIVKENCBLKANREK---CGWTGSTCVDIVCTTAPTAKTDD-----D 603
QY 121 YTVBECTC-----EDCIKSKPKVDSHCFPLPAMEEGATI-----LVTTKTN 162
Db 604 YTVELCEAYKPSNCV---PNGTKGCMELAAKCESRTIKEQCDVAGTKTN 651

RESULT 7
D89010
protein R08F11.7 (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89010
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D89010
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-773 <STO>
A;Cross-references: UNIPROT:O01892; GB:chr_V; PIDN:AAB54249.1; PID:G2088832; GSPDB:GN0002
A;Note: Similar to peroxidase
C;Genetics:
A;Gene: R08F11.7
A;Map position: 5
C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 8.4%; Score 81; DB 2; Length 773;
Best Local Similarity 21.7%; Pred. No. 17;
Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;
QY 23 PCQLRCSSNTPLTTCQ-----RYCN-----ASVTNSVKGTTNAILWTCL---GLSL 64
Db 184 PPKSNATCQGPCKSCSDPVHDIRSITGYCNRKPKTQANSVTAIRLLGTTTSYTDGLOA 243
QY 65 IISLAVFVLMFLLRKISSSEPLKDEFKNTG-SGLLGMANIDLEKSGRTGDEIILPRGLETV 123
Db 244 IRTSVTGSPLPSTRILISNKLHDEGSTPNFSPSVNHLHMQIGQFIADHIFMPSSTAKOG 303
QY 124 EECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE 176
Db 304 SSLNCTSC--SSPTTISTNCAPIPADDKYFTFPVSRTEARCIRLRLTALNGSGSGFVRTQ 361
QY 177 IEKS 180
Db 362 IDQN 365

RESULT 8

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-539 <ARN>
A;Cross-references: UNIPROT:Q9XON0; GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD3622
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
Best Local Similarity 32.0%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5;

Qy 42 NASVTNSVKGTNAIITWCLGSLIISLAVFVLMFLRKISSEPLKD---EFKNTGSGLLG 98
Db 150 NVSMTKNIK-RNIIF---LVVVCAAAMFTAITETRLTT-PLKLAIVLVENLSHGVL- 202

Qy 99 MANIDLEKSRGDEI 113
Db 203 --NVEIEKIRSKDEI 215

RESULT 16
T21152
hypothetical protein F20E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21152
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19383
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-357 <WIL>
A;Cross-references: UNIPROT:Q9XV87; EMBL:Z81508; PIDN:CAB04138.1; GSPDB:GNO0023; CESP:F20E11
A;Experimental source: clone F20E11
C;Genetics:
A;Gene: CESP:F20E11.7
A;Map position: 5
A;Introns: 52/3; 88/2; 103/3; 154/3; 190/2; 205/3; 241/2; 270/3; 321/3

Query Match 7.9%; Score 76.5; DB 2; Length 357;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 45; Conservative 33; Mismatches 66; Indels 63; Gaps 10;

Qy 20 ACIPQCLRCSSNTPLTCQRYCNAS-----VTNSVKGTNAIITWCLGSLIISLAVF 71
Db 102 SCLPCQ-TCAPPTDPMSEKATCTATPGTDCATLAVKCMINAGPDCNDVALLIQTGG 160

Qy 72 VLMP-----LURKISSEPLKD-----EFKNTGSGLL 96
Db 161 ALPTGTGPGQIAETSVTCGDKDIQDPNGIRGNTLIASIASETCLEMTGGLFTSGTP 220

Qy 97 LGWANIDLEKSR--GDIRII--PRG-----LEVVECTCEDCIKS-----KPKVDSHC 143
Db 221 GPFA-----ETSVTCGDDVILQDPNGTRGNTLIASITATQTCVSCMQTWRILKRLGRLPQC 276

Qy 144 --FPLPAMEGATILVTTKTNDYCKSL 168
Db 277 TAFMDPWVPEATCTVTGVTSGACATL 303

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-539 <ARN>
A;Cross-references: UNIPROT:Q9XON0; GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD3622
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein

RESULT 17
T19277
hypothetical protein C14B4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19277; T19909
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19100
A;Accession: T19277
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1404 <WIL>
A;Cross-references: UNIPROT:O45251; EMBL:Z81471; PIDN:CAB03887.1; GSPDB:GNO0023; CESP:C14B4.2
A;Experimental source: clone C14B4
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19194
A;Accession: T19909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1404 <WIL>
A;Cross-references: EMBL:Z81483; PIDN:CAB03966.1; GSPDB:GNO0023; CESP:C14B4.2
A;Experimental source: clone C43D7
C;Genetics:
A;Gene: CESP:C14B4.2
A;Map position: 5
A;Introns: 175/1; 209/3; 304/2; 482/3; 611/3; 680/1; 787/1; 1048/3; 1112/2; 1197/2; 1237/2; 1237/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C14B4.2

Query Match 7.9%; Score 76.5; DB 2; Length 1404;
Best Local Similarity 24.8%; Pred. No. 81;
Matches 35; Conservative 21; Mismatches 56; Indels 29; Gaps 6;

Qy 2 LQWAGCCSQNEYFDSLIH--ACIPQCLRCSSNTPLTCQRYC-----NASVTN-SVKGTNA 54
Db 77 LIFSFGCHVEQDPLVLDQSAHFNGSRTEAHLRLTCKGYCTVGSGMTVTDLSIYYRNE 136

Qy 55 ILWTCLGLSLIISLAVFVLMFLRKISSEPLKDFTKNTG-----SGLLGMANIDLEKSRGT 110
Db 137 LIITCTGKVLVIG-----DSDVITCFRNDALWQVEKNLKNWTGSIQSESDG 183

Qy 111 DEILPRGLEVTVECTCEDC 131
Db 184 TIFV-----KYSMNIVLHEDC 199

RESULT 18
A43353
ascites sialoglycoprotein-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43353
R;Sheng, Z.; Wu, K.; Carraway, K.L.; Fregien, N.
J. Biol. Chem. 267, 16341-16346, 1992
A;Title: Molecular cloning of the transmembrane component of the 13762 mammary adenocarcinoma
A;Reference number: A43353; MUID:92355597; PMID:1379596
A;Accession: A43353
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-744 <SHE>
A;Cross-references: UNIPROT:Q63661
A;Experimental source: mammary adenocarcinoma
A;Note: sequence extracted from NCBI backbone (NCBI:110690, NCBI:110691)
C;Keywords: glycoprotein
F;655-694/Domain: EGF homology <EGF>

Query Match 7.9%; Score 76; DB 2; Length 744;
Best Local Similarity 22.1%; Pred. No. 47;
Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6;

Qy 4 MAGCCSQNEYFDSLIHACIPQCLRCSSNTPLTCQRYC-----NASVTNSVKGT 52

Db 49 LGRTRAGTDSANATNFIAFAAQNTSSLSKSPITVQWFLEPNDRIRVVHNNQTVAFNTSDT 108
QY 53 NAI-LWTCGLSLI-----ISLAVFLMFLRLKISSEPLKDFKNTGSLG 98
Db 109 EDLPVFNATGVLLIQGQSVAFNFGVTIVSIALSNILHASS--LSEBYRNHTKGLG 166
QY 99 MANIDKSTGTDEIILPRGLVTVVECTCEDCI 132
Db 167 VWNDNPE-----DDFRMPNG--STIPSNNTSEETL 193
RESULT 19
T41478
complex I intermediate-associated protein CIA84 precursor, mitochondrial [imported] - Ne
C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47250
R;Kuffner, R.; Rohr, A.; Schmiede, A.; Krull, C.; Schulte, U.
J. Mol. Biol. 283, 409-17, 1998
A;Title: Involvement of two novel chaperones in the assembly of mitochondrial NADH:Ubiqu
A;Reference number: 222191; PMID:9769214; PMID:9769214
A;Accession: T47250
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-748 <KOE>
A;Cross-references: UNIPROT:O42637; EMBL:AJ001712; PIDN:CAA04945.1
C;Genetics:
A;Gene: cia84
A;Genome: nuclear
A;Introns: 693/2
C;Function:
A;Description: required for complex I membrane arm assembly
C;Superfamily: Neurospora crassa complex I intermediate-associated protein CIA84
C;Keywords: mitochondrion
F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;1-748/Product: complex I intermediate associated protein CIA84 #status predicted <MA

Query Match 7.9%; Score 76; DB 2; Length 748;
Best Local Similarity 25.5%; Pred. No. 47;
Matches 27; Conservative 20; Mismatches 49; Indels 10; Gaps 2;
QY 82 SEPLKDFKNTGSLGQMANIDLEKRTGDEIILPRGLVTVVECTCEDCIKPKVDSD 141
Db 266 SKPIHGSPGTGLLELVRSRRSQKNWLLP-----VFEVQVQDFAKKGLDAF 319
QY 142 HCPPLPAMEG---ATILVTTNDYCKSLPAALGATEIEKISA 183
Db 320 LQSVLALDKGPGIKTYLQTMASGDFYQSHSVKVDATTINRLMQA 365
RESULT 20
T41478
probable transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41478
R;Bothe, G.; Pohl, T.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: 221997
A;Accession: T41478
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-638 <BOT>
A;Cross-references: UNIPROT:O74910; EMBL:AL031644; PIDN:CAA21064.1; GSPDB:GN00068; SPDB:
C;Genetics:
A;Experimental source: strain 972h-; cosmid c613
A;Gene: SPDB:SPCC613.12C
A;Map position: 3
C;Superfamily: Schizosaccharomyces pombe probable transcription regulator SPCC613.12C

Query Match 7.8%; Score 75.5; DB 2; Length 638;
Best Local Similarity 22.7%; Pred. No. 45;
Matches 44; Conservative 20; Mismatches 61; Indels 69; Gaps 7;
QY 12 EYPDSLLHACIPQQLRCSSNTPLTCQRYCNASVTNSVKGNTNAILWTCLGLSLIISLAVF 71
Db 42 EIYDPPYRAELPCP-----KPSLSISKHSIAKVPNSVNR-----LEQLLLTSGTF 88
QY 72 VLMFLRLKISSEPLKDFKNTGSLGQMANIDLEKRTGDEIILPRGLVTVVECT 126
Db 89 L-----PNSRPYLSEVRVKHTL-----LSNSITGDKPSLIHVDTPBECFILQE 134
QY 127 -----TCEDCIKPKVDSDHCFPLPAMEGATILVT 158
Db 135 AKLFGPVNSVQFNDAVSTHSPKLPRAVEDC-----QKFEIDNPSLSPVDKHAIIIRT 190
QY 159 TKTN-----DYCKS 167
Db 191 YKKNKLLPDYLS 204
RESULT 21
B97297
hydrogenase chain (ferredoxin) [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97297
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; PMID:21359325; PMID:21359325
A;Accession: B97297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <KUR>
A;Cross-references: UNIPROT:Q97E85; GB:AE001437; PIDN:AAK81165.1; PID:g15026303; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3230

Query Match 7.8%; Score 75; DB 2; Length 450;
Best Local Similarity 20.5%; Pred. No. 35;
Matches 42; Conservative 23; Mismatches 72; Indels 68; Gaps 9;
QY 15 DSHLHACIPQQLRCSSNTPLTCQRYC--NASVTNSVKGNTNAIL-----LWTCGL 61
Db 74 DNIVEIKEDCSSCHSNEGETPCQKSCFPDAILVDKNTKTSHTQDLCTDGCNCITSCPS 133
QY 62 LSLIISLAVFLMFLRLKISSEPLKDFKNTGSLGMA-----NIDLEKSR----- 109
Db 134 GS-----ILDKIEFMLELNFKNNTVIAAPAIAGQFGENVSLMLRTAFK 181
QY 110 -----GDEIILPRGLEVT-----VECTCEDCIKPKVDSD---HC 143
Db 182 KVGFDAMVEVAFADMLTIKEAFEPNELVNSKDDLMITSCCPMWVSMIRKIYKDLARHV 241
QY 144 FP--LPAMEGATILVTTNDYCK 166
Db 242 SPVSVPMIASGRVI---KKLNPCK 263
RESULT 22
A41369
S-receptor kinase (EC 2.7.1.1) 6 precursor - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 11-Jun-1999
C;Accession: A41369
R;Stein, J.C.; Howlett, B.; Boyes, D.C.; Nasrallah, M.E.; Nasrallah, J.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 8816-8820, 1991
A;Title: Molecular cloning of a putative receptor protein kinase gene encoded at the self
A;Reference number: A41369; PMID:92020942; PMID:1681543
A;Accession: A41369
A;Molecule type: DNA
A;Residues: 1-857 <STE>
A;Cross-references: GB:M76647; NID:g167166; PIDN:AAA33000.1; PID:g167167.

A;Experimental source: S6S6 homozygote kale

C;Genetics:

A;Gene: SRK

A;Note: locus is highly polymorphic

C;Function:

A;Description: involved in preventing fertilization between plants having the same S-locus
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
C;Keywords: ATP; glycoprotein; magnesium; phosphotransferase; receptor; serine/threonine
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-857/Product: S-receptor kinase #status predicted <MA>
F;41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F;447-466/Domain: transmembrane #status predicted <TM>
F;526-813/Domain: protein kinase homology <KIN>
F;534-542/Region: protein kinase ATP-binding motif
F;47,120,196,260,314,389,442/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;556,572,653,655/Active site: Lys, Glu, Asp, Lys #status predicted
F;659,662/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 7.8%; Score 75; DB 1; Length 857;

Best Local Similarity 17.6%; Pred. No. 67;

Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

Qy 24 COLRCSSNTPPLTCQRYCNASVTNSVKGNTNAILWT----- 58

Db 380 CKKRCISD---CNCATFANADIRNG--GSGCVIWELEDIRNVATDAIDGQDIYVRLAA 434

Qy 59 -----CLGLSLIIISLAVFLVLMFLIRKISBPLKDEPKNTGSGLLGMANIDLEK 106

Db 435 ADIAKKRNASGKIISLTGVSVLLIMFCL-----WKRKQKRAKASALSANTQNRQ 487

Qy 107 SRTGDEIILPGLLEYVEECTCECIKSPKVDSDHCP-----PLPAMEGATILVTYTKT 161

Db 488 NLPNMWVL-----SSKREFSGEYKFELELPIEME---TVVKATEN 527

Qy 162 NDYCKSL 168

Db 528 FSSCNKL 534

RESULT 23

S45592

ERD1 protein - yeast (Kluyveromyces marxianus var. lactis)

C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica

C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S45592

R;Dean, N.

Yeast 10, 1117-1124, 1994

A;Title: Cloning and DNA sequence of a Kluyveromyces lactis ERD1 homologue.

A;Reference number: S45592; MUID:95084639; PMID:7992512

A;Accession: S45592

A;Molecule type: DNA

A;Residues: 1-384 <DEA>

A;Cross-references: UNIPROT:P41771; EMBL:U04714; NID:G436876; PIDN:AAA21530.1; PID:G4368

A;Note: the source is designated as Kluyveromyces lactis

C;Genetics:

A;Gene: ERD1

Query Match

Best Local Similarity 7.7%; Score 74.5; DB 2; Length 384;

Matches 43; Conservative 21; Mismatches 55; Indels 39; Gaps 8;

Qy 9 SONEFYFSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGNTNAILWTCLGLSLIISL 68

Db 67 SSLKLFKISIRVIIPWQLVC-----IILFQY---SFTNNV---SNKLLWFFLNVSPLEL 115

Qy 69 AVFVLMFLRKISSEPLKDEPKNTGSGLLGMANIDLEKSTGDEIILPGLLEYVEECTC 128

Db 116 -FYFAMILR--SSAMVARCFKR-----ILWVADIEPKPYRNVIISDTLTSY----- 161

Qy 129 EDCIKSPKVDSDHCFPLPAMEGATILVTYTKNDYCK 166

Db 162 ----SKFLVD-----LAIYATFLFHDPTNVKQ 185

RESULT 24

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T16840

R;Geisel, C.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid T10E10.

A;Reference number: Z18588

A;Accession: T16840

A;Status: preliminary; translated from GB/EMBL/DDBU

A;Molecule type: DNA

A;Residues: 1-1101 <GEI>

A;Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:G1049343; PIDN:AAA803

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T10E10.4

A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 76/3;

Query Match

Best Local Similarity 7.7%; Score 74.5; DB 2; Length 1101;

Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;

Qy 7 QCSQNEYFDSLLHACIPCOLR--CSSNTPLTTCQRYCNASVTNSVKGNTN 53

Db 350 QCSQSTVFNSDLNVCVPLAIQNSDSSSTQQPVCs--C-SQVSSSCPPTS 395

RESULT 25

JC7535

chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus

C;Species: Streptomyces thermoviolaceus

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C;Accession: JC7535

R;Tsujibo, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inanami

Biosci. Biotechnol. Biochem. 64, 2445-2453, 2000

A;Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular cloning

A;Reference number: JC7535; MUID:21036907; PMID:11193414

A;Accession: JC7535

A;Molecule type: DNA

A;Residues: 1-377 <TSU>

A;Cross-references: UNIPROT:Q9RHU5; DBU:AB016842

A;Experimental source: strain OPC-520

C;Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation

lysaccharide-binding domain that is important in the efficient hydrolysis of insoluble chitin

C;Genetics:

A;Gene: chi35

C;Keywords: glycosidase; hydrolase

Query Match

Best Local Similarity 7.7%; Score 74; DB 2; Length 377;

Matches 31; Conservative 11; Mismatches 23; Indels 50; Gaps 6;

Qy 47 NSVKGNTNAILWTCLGLS-----LIISLAVFLVLMF-----L 76

Db 138 NSANGTRVQIWTCTGGSNQKNAPATGGSTPAPSGFVVSEAFQNFNPNFPYTVQGL 197

Qy 77 LRKISSEPLKDEPKNTG-----SGLLGMANIDLEKSTGDEIILPGLLEYTVE 124

Db 198 VQALSAPP---GPANTGDDTTKQEAFAFLANVNH---TG-----GLQYVVE 239

RESULT 26

B95099

membrane protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: B95099

R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Mayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <KUR>
A;Cross-references: UNIPROT:Q97RG2; UNIPROT:Q8DQB0; GB:AE005672; PIDN:AAK74987.1; PID:gl
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0859

Query Match 7.6%; Score 73.5; DB 2; Length 307;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

QY 1 MLQAGCQSQNEFYDLSLHACIPQLRCSSNTPLTCQRYCN-ASVTSVK-CTNAILWT 58
Db 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRLGTS-A-FWT 44
QY 59 CIGLSLI-----ISLAVFLMFLLR-----KISSEPLKDFKNTGSGLLGMANIDLE 105
Db 45 LLSITFIGGSMYMNMSIGIIVILLSLTLPKQVRIGTLPSLDWK-----ANI--E 93

QY 106 KSRTGDEIILPRGLEIYTVBECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYC 165
Db 94 SNRLKNKIFIPVML-MAILALVLAQMIPFSKIS----ISLAAL--PATISVLVITNSHP 146

QY 166 KSL 168
Db 147 KSL 149

RESULT 27
A97967
conserved hypothetical protein spr0761 [imported] - *Streptococcus pneumoniae* (strain R6)
C;Species: *Streptococcus pneumoniae*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
A;Accession: A97967
R;Authors: J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A97967
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <KUR>
A;Cross-references: UNIPROT:Q97RG2; UNIPROT:Q8DQB0; GB:AE007317; PIDN:AAK99565.1; PID:gl
A;Genetics:
A;Gene: spr0761

Query Match 7.6%; Score 73.5; DB 2; Length 307;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

QY 1 MLQAGCQSQNEFYDLSLHACIPQLRCSSNTPLTCQRYCN-ASVTSVK-CTNAILWT 58
Db 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRLGTS-A-FWT 44
QY 59 CIGLSLI-----ISLAVFLMFLLR-----KISSEPLKDFKNTGSGLLGMANIDLE 105
Db 45 LLSITFIGGSMYMNMSIGIIVILLSLTLPKQVRIGTLPSLDWK-----ANI--E 93

QY 106 KSRTGDEIILPRGLEIYTVBECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYC 165
Db 94 SNRLKNKIFIPVML-MAILALVLAQMIPFSKIS----ISLAAL--PATISVLVITNSHP 146

QY 166 KSL 168
Db 147 KSL 149

Db 147 KSL 149

RESULT 28
A89882
hypothetical protein ctab [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A;Accession: A89882
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89882
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <KUR>
A;Cross-references: UNIPROT:Q99UV7; GB:BA000018; PID:gl3700917; PIDN:BA842213.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: ctab
C;Superfamily: heme O synthase

Query Match 7.6%; Score 73; DB 2; Length 304;
Best Local Similarity 23.8%; Pred. No. 36;
Matches 24; Conservative 16; Mismatches 29; Indels 32; Gaps 4;

QY 2 LQWAGCQSQNEFYDLSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGTNAILWTCLG 61
Db 67 LIMGACALNNYYDQIDRIMPSK-----QNRP-----TVNNRITDONLLLS-FG 111

QY 62 LSLIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANI 102
Db 112 MMLVSGICIFLL-----NIPSGVLGMCI 135

RESULT 29
B96599
protein P20N2.12 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A;Accession: B96599
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-679 <STO>
A;Cross-references: UNIPROT:Q9ZWD7; GB:AE005173; MID:g8778489; PIDN:AAF79497.1; GSPDB:G
C;Genetics:
A;Gene: F20N2.12
A;Map position: 1

Query Match 7.6%; Score 73; DB 2; Length 679;
Best Local Similarity 22.2%; Pred. No. 81;
Matches 35; Conservative 21; Mismatches 58; Indels 44; Gaps 8;

QY 7 QCSQNEFYDLSLHACIPQ-----LRCSNTP-----PLTCQRYC 41
Db 199 KCQTNLQEVYH-CSICKENLNTCARNPPLSTISHLKSHEHPLSPFRPRLPCDA-C 256

QY 42 NASVTSVKGTNAILWTCLGSLIISLAVFLMFLLR-----KISSEPLKDFKNTGSG 95

hypothetical protein F313.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10543
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voickaert, G.; Ba
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17080
A;Accession: T10543
A;Molecule type: DNA
A;Residues: 1-500 <BEV>
A;Cross-references: UNIPROT:Q95V26; EMBL:AL080237; GSPDB:GN00062; ATSP:F313.50
A;Experimental source: cultivar Columbia; BAC clone F313
C;Genetics:
A;Gene: ATSP:F313.50
A;Map position: 4

Query Match 7.4%; Score 71; DB 2; Length 500;
Best Local Similarity 23.6%; Pred. No. 91;
Matches 33; Conservative 17; Mismatches 52; Indels 38; Gaps 7;

Qy 16 SLHA-----CIPQLRCSSNPPLTCQRYCNASVTNS-----VKGTNAILMTCLG 61
Db 142 SLHSGKEVGFCLRNKLCIDAVYATVDMYKSGDLQSAIEIFWGIKNKSLASWNCML 201

Qy 62 LSLII-----SLAVFVFLRLKISSEPLKDFE-----KNTGSLGLGMANIDLEKSR 108
Db 202 MGYAMFGREGIEAFAFVML---EAGMEPDAITFTSVLSVCKNSGLVQEGWKYFDLMRSR 258

Qy 109 TGDIEIILPRGLEVTVECTC 128
Db 259 YG---IIP-----TIEHCSC 270

RESULT 42
T02768
spike glycoprotein G homolog - Adelaide River virus
C;Species: Adelaide River virus
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T02768
R;Wang, Y.; Walker, P.J.
Virology 195, 719-731, 1993
A;Title: Adelaide river rhabdovirus expresses consecutive glycoprotein genes as polycist
A;Reference number: Z14732; MUID:9331730; PMID:8337841
A;Accession: T02768
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: genomic RNA
A;Residues: 1-660 <WANG>
A;Cross-references: UNIPROT:Q89669; EMBL:L09206; NID:g348027; PIDN:AAA02762.1; PID:g3480
A;Experimental source: isolate DPP61
C;Superfamily: rhabdovirus spike glycoprotein G

Query Match 7.4%; Score 71; DB 2; Length 660;
Best Local Similarity 32.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

Qy 57 WTCIGLSLIISL-AVFVLMFLRLKISSEPLKDFEKT-GSGLGLGMANIDLEKSR 109
Db 558 WTWGVGLFSITFLYKIIMLRKHSNDNVKFEKETAGKVMIGQPIDTKSMRST 612

RESULT 43
H82933
hypothetical protein UUI01 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: H82933
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-188 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6999051; PIDN:AAF30507.1; GSPDB:GN001;
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UUI01
A;Genetic code: SGC3

Query Match 7.3%; Score 70.5; DB 2; Length 188;
Best Local Similarity 25.5%; Pred. No. 37;
Matches 27; Conservative 19; Mismatches 39; Indels 21; Gaps 4;

Qy 51 GTNAILWTCIGLSLIISLAVFV---LMFLRLKISSEPLKDFEKTGSGLLGMANIDLEKS 107
Db 35-GDEAYKTSGLGSELYINADFESTNILDKBELOAKIDAFILISNDTVLIDSEVFLDIH 94

Qy 108 RTGDEIILPRGLEVTVECTCED-----CIKSKPKVDSDDHC 143
Db 95 FSEDD-----DYE-EDCCDECCSDENEACCNSEKVEECC 132

RESULT 44
T24023
hypothetical protein R07B7.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 13-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T24023
R;Harris, B.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19830
A;Accession: T24023
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-412 <WIL>
A;Cross-references: UNIPROT:Q21806; EMBL:Z75955; PIDN:CAB00125.1; GSPDB:GN00023; CESP:RO
A;Experimental source: clone R07B7
C;Genetics:
A;Gene: CESP:R07B7.16
A;Map position: 5
A;Introns: 26/3; 53/3; 89/1; 139/3; 203/2; 325/1
C;Superfamily: erba transforming protein homology

Query Match 7.3%; Score 70.5; DB 2; Length 412;
Best Local Similarity 19.6%; Pred. No. 83;
Matches 36; Conservative 32; Mismatches 69; Indels 47; Gaps 9;

Qy 11 NEYFDSLHACIPCQLRCSSNPPLTCQRYCNASVTNSVKGTVNAILWTCIGLSLIISLAV 70
Db 186 NFVFDs---SRIPNLTPVSNKAPKLCIMTYMHSALLAAVEASKT-----PEFFFSKISH 235

Qy 71 FVLMFLRLKISSEPLKDFEKTGSGLLGMANIDLEKSRGTGDEIILPRGLEY-TVEECTCE 129
Db 236 EARMILIRHVSL-----IGSNMMS-ASPSMH-HRKSDELLLPDGTVFGSIGGCLAS 284

Qy 130 DC---IKSKPKVDS-DHCF-----PLPAMEGATILVTTKNDY 164
Db 285 EVLGEIKYKNQLOOILHAFILRNVDREYVMILKAILMRNPSVPLGLTDOLIENERNOY 344

Qy 165 CKSL 168
Db 345 AKAL 348

RESULT 45
T14525
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14525
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class
A;Molecule type: DNA

A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Accession: T14525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-424 <KUS>
A;Cross-references: UNIPROT:O3834; EMBL:D85200; NID:g2351131; PIDN:BAA21934.1; PID:g235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match 7.3%; Score 70.5; DB 2; Length 424;
Best Local Similarity 40.0%; Pred. No. 85;
Matches 14; Conservative 5; Mismatches 11; Indels 5; Gaps 2;

QY 24 CQLRCSSTPPLTCQRYCNASVTNSVKGITNAILWT 58
Db 369 CERKCLSD---CNCAYANADIENS--GTGCVIWT 398

RESULT 46

T32003

hypothetical protein F36H9.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T32003

R;Dante, M.; Kramer, J.; Twyman, B.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of C. elegans cosmid F36H9.

A;Reference number: Z21110

A;Accession: T32003

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-490 <DAN>

A;Cross-references: EMBL:AF016668; PIDN:AAB66095.1; GSPDB:GN00020; CESP:F36H9.4

A;Experimental source: strain Bristol N2; clone F36H9

C;Genetics:

A;Gene: CESP:F36H9.4

A;Map position: 2

A;Introns: 5/3; 22/1; 46/3; 72/3; 199/2; 220/3; 278/3; 306/2; 345/3; 427/3

Query Match 7.3%; Score 70.5; DB 2; Length 490;

Best Local Similarity 21.3%; Pred. No. 99;

Matches 49; Conservative 23; Mismatches 65; Indels 93; Gaps 12;

QY 2 LOMAGQSQNEYFDSLHACIPQLRCSSTPPLT--C-----QRYCNASVTNS 48
Db 271 LSIIGHKADGTY-----VEKCAEKTDDLTOGGINIGIRGIAAKQCLCKTDL 321

QY 49 VKGTNAILWTCLGLSL-----IISLAV---FVIMFLLRKISSEPLKDE--FKNTG 93
Db 322 SPQGP--FRTCLGLGLGLFYAFWRIIISFLMPTNFYAYFLMPKFQVLPILNSQVSKYT- 378

QY 94 SGLLGMANIDLEKSRGTDEIILPRGLETVVECTCEDCIKSKPK----- 137
Db 379 -----LRVKPDARSAPRNLR-----CLTRERKQILFVNRNFSIFLLPF 417

QY 138 VDSHDCPP-----LPAM-EGCATILVTTKNDYCKSLPAA 171

Db 418 FKNDHRDFNFSICNKKLENLJLALFRSFLSLFCISASSDLCKSCPA 467

RESULT 47

S54174

DNA topoisomerase (EC 5.99.1.2) - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54174

R;Tosh, K.T.; Kilbey, B.J.K.

submitted to the EMBL Data Library, January 1995

A;Description: Isolation and characterisation of the topoisomerase 1 gene from Plasmodium

A;Reference number: S54174

A;Accession: S54174

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-839 <TOS>

A;Cross-references: UNIPROT:Q26024; UNIPROT:Q81329; EMBL:X83758; NID:g790481; PID:g790481

C;Superfamily: eukaryotic type I DNA topoisomerase

C;Keywords: DNA binding; DNA replication; isomerase

Query Match 7.3%; Score 70.5; DB 2; Length 839;

Best Local Similarity 21.8%; Pred. No. 1.7e+02;

Matches 37; Conservative 26; Mismatches 69; Indels 39; Gaps 5;

QY 36 TCQRYCNASVTNSVKGITNAILWTCLGLSLIISLAVFVLMFLMRKISSEPLKDFKNT- 94
Db 403 SCVHKIREDYKKNKKNII-----DKQLGTAVLIDFLALRVGGERKIDDEADTVGC 455

QY 95 GLIGMANI-----DLEKSRGTDEIILPRGLETVVECTCEDCIKSKPKV--DSD 141
Db 456 CSLRVEHIGFAHDIPFKSVDSKEQTKNDKVNKIPLPTNLESISSEDCYITLDFLGKDSI 515

QY 142 HCFPLPAMEGATI-----LVTTKTNDYCKSLPAALSA 174

Db 516 RYENTVKIDQAYINIIIFCKNNRDEGVDFDQITCKSLNEYLKEIMPTLSA 566

RESULT 48

T01440

hypothetical protein F24O1.2 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01440

R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con-

eclogis, A.; Ecker, J.R.

submitted to the EMBL Data Library, January 1998

A;Description: Genomic sequence for Arabidopsis thaliana BAC F24O1.

A;Reference number: Z14211

A;Accession: T01440

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-906 <SHI>

A;Cross-references: UNIPROT:O48794; EMBL:AC003113; NID:g2689438; PID:g2781345; GSPDB:GN00

C;Genetics:

A;Gene: ATSP:F24O1.2

A;Map position: 1

A;Introns: 239/2; 272/3; 317/1; 338/2; 682/3; 832/1; 860/3

Query Match 7.3%; Score 70.5; DB 2; Length 906;

Best Local Similarity 20.9%; Pred. No. 1.8e+02;

Matches 37; Conservative 19; Mismatches 54; Indels 67; Gaps 7;

QY 7 QCSQNEYFDSLHACIPQ-----LRCSSTPP-----LTCQRYCNASVTNSVK 50
Db 211 QCLKGERITLLI--CSECEKTMFCQIRKWPNLSEDDVVEKPLCRQNCNC----- 262

QY 51 GTNAILWTCLGLSLIIS-----LAVFVLMFLLRKISSEPLKDFKNTG 93
Db 263 -----KCHLHNGLETSKRELAKSERRHQLQYLITLMPFLNKLISFQKLEIEFATV 315

QY 94 SGLLGMANIDLEKSRGTDEIILPRGLETVVECTCEDCI-----KSKPKVDSHCH 143
Db 316 QGKL-----PSEVEITAAISYTDERVYCDHCATSIVDLHRSCPKCYELC 360

RESULT 49

A42916

metabotropic glutamate receptor mGluR5 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42916

R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.

J. Biol. Chem. 267, 13361-13368, 1992

A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5

A;Reference number: A42916; MUID:92317054; PMID:1320017

A;Accession: A42916

A;Status: preliminary

A;Molecule type: mRNA

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:44:33 ; Search time 214.385 Seconds
(without alignments)
493.825 Million cell updates/sec

Title: US-10-077-137-1
Perfect score: 964
Sequence: 1 MIQMACQCSQNEYFDSLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	964	100.0	184	1	TR17_HUMAN	Q02223 homo sapien
2	960	99.6	184	2	O6PE46	G6pe46 homo sapien
3	960	99.6	184	2	AH58291	Ah58291 homo sapi
4	572	59.3	185	1	TR17_MOUSE	O88472 mus musculu
5	116.5	12.1	175	1	T13C_MOUSE	Q9d8d0 mus musculu
6	116.5	12.1	175	2	Q8R4W8	Q8r4w8 mus musculu
7	94	9.8	323	1	TNR6_BOVIN	P51867 bos taurus
8	93	9.6	184	1	T13C_HUMAN	Q96tj3 homo sapien
9	92.5	9.6	334	2	O6VT98	O6vt98 symbiont ba
10	92.5	9.6	334	2	AAS47559	Aas47559 symbiont
11	89	9.2	3005	2	O6BFG4	O6bfg4 paramecium
12	88.5	9.2	217	2	Q97D61	Q97d61 clostridium
13	86.5	9.0	804	2	O80XB3	O80xb3 mus musculu
14	86.5	9.0	809	2	O80XB2	O80xb2 mus musculu
15	86.5	9.0	823	2	O80XB6	O80xb6 mus musculu
16	86.5	9.0	827	2	Q8CDK8	Q8cdk8 mus musculu
17	86.5	9.0	834	2	Q8BH12	Q8bh12 mus musculu
18	86.5	9.0	842	2	Q8R056	Q8r056 mus musculu
19	86.5	9.0	867	1	PML1_MOUSE	O54990 mus musculu
20	86	8.9	1309	2	O6CCL1	O6ccl1 yarrowia li
21	85.5	8.9	1193	2	O9Y1X8	O9y1x8 ephydatia f
22	83.5	8.7	938	2	Q8RWV7	Q8rvw7 arabidopsis
23	83.5	8.7	1998	2	Q9STR8	Q9str8 arabidopsis
24	83	8.6	449	2	Q8C8R5	Q8c8r5 mus musculu
25	83	8.6	474	2	Q8C9L4	Q8c9l4 mus musculu
26	82.5	8.6	164	2	Q7RAA5	Q7raa5 plasmodium
27	82.5	8.6	1142	2	O6CCL7	O6ccl7 yarrowia li
28	82	8.5	327	2	O97491	O97491 oviss aries
29	82	8.5	967	2	Q8C2G0	Q8c2g0 mus musculu
30	82	8.5	1009	1	FAK2_MOUSE	Q9qvp9 m protein t
31	82	8.5	1009	1	FAK2_RAT	P70600 rattus norv

ALIGNMENTS

Q8vev6	mus musculu	314	2	Q8VEV6
Q94711	paramecium	2233	2	Q94711
Q39191	arabidopsis	595	2	Q39191
O01892	caenorhabdi	773	2	O01892
O7tcg9	mus musculu	81	2	O7TCQ9
O8in99	drosofila	487	2	O8IN99
O81820	arabidopsis	735	2	O81820
O8kly1	pseudomonas	153	2	O8KLY1
Q14289	h protein t	1009	1	FAK2_HUMAN
O6pid4	homo sapien	1009	2	O6PID4
Aah36651	homo sapi	1009	2	AAH36651
Q26489	spodoptera	1299	2	Q26489
Q7r6v0	plasmodium	333	2	Q7R6V0
Q80281	fugu rubrip	1200	2	Q802S1
O81836	homo sapien	293	1	T13X_HUMAN
O8vf0	mus musculu	314	2	O8VFW0
O58752	methanococ	343	1	MJK2_METJA
Q9h677	homo sapien	485	2	Q9HC77
Q8n6t0	homo sapien	522	2	Q8N6T0
Q8lq43	oryza sativ	789	2	O8LQ43
O8r221	mus musculu	841	2	O8R221
O81819	arabidopsis	738	2	O81819
Q9lmn6	arabidopsis	738	2	Q9LMN6
Q9yku7	human immun	853	2	Q9YKU7
O04623	arabidopsis	968	2	O04623
Q9et35	mus musculu	249	1	T13X_MOUSE
O6bu93	debaromyce	399	2	O6BU93
Q9m3b3	arabidopsis	522	2	Q9M3B3
Q9x0n0	thermotoga	539	2	Q9X0N0
O6csu4	kluyveromyc	2149	2	O6CSU4
Q9xv87	caenorhabdi	357	2	Q9XV87
Q9fj63	arabidopsis	656	2	Q9FJ63
O45251	caenorhabdi	1404	2	O45251
O6lhf6	photobacter	465	2	O6LHF6
Cag23274	photobact	465	2	CAG23274
Q7nhb6	mycoplasma	566	2	Q7NBH6
O42637	neutrospora	748	1	C184_NEUCR
Q78206	neutrospora	759	2	Q7S820
Q7rm66	plasmodium	1255	2	Q7RM66
O63661	rattus norv	1805	2	O63661
Q7qir6	giardia lam	191	2	Q7QIR6
Q8d6l4	vibrio vuln	202	2	Q8D6L4
Q76nx0	dictyosteli	454	2	Q76NX0
Aam09326	dictyoste	454	2	AAM09326
O6fj19	candida gla	476	2	O6FQJ9
O8jkv7	heliobact	567	2	O8JKV7
Q74910	schizosacch	638	1	YCSB_SCHPO
Q97e85	clostridium	450	2	Q97E85
Q86h21	dictyosteli	706	2	Q86H21
Q9bi07	entamoeba h	718	2	Q9BI07
O09092	brassica ol	849	1	SRK6_BRAOL
O6fk14	candida gla	920	2	O6FK14
Q7z5t8	homo sapien	985	2	Q7Z5T8
Q81z06	homo sapien	985	2	Q81Z06
O6fkt2	candida gla	1193	2	O6FKT2
O6w4x9	homo sapien	1569	2	O6W4X9
AaQ82434	homo sapi	1569	2	AAQ82434
Q8c3k1	mus musculu	263	2	Q8C3K1
P41771	kluyveromyc	384	1	ERD1_KLUJLA
Q7ztml	xenopus lae	521	2	Q7ZTML
Q9qv47	giardia lam	660	2	Q9QV47
Q9ykv7	human immun	777	2	Q9YKV7
Q22378	caenorhabdi	966	2	Q22378
Q7qta2	giardia lam	2199	2	Q7QTX2
Q8kmk7	mycoplasma	353	2	Q8KMK7
Q9rh05	streptomyce	377	2	Q9RHU5
Q91000	gallus gall	789	2	Q91000
Q8nfy8	homo sapien	2371	2	Q8NFY8

RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.,
 RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 RL autoimmune disease."; Nature 404:995-999(2000).
 RN [6]
 RN FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
 RP Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RL humoral immunity."; Nat. Immunol. 1:252-256(2000).
 RN [9]
 RN INTERACTIONS WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
 RP Shu H.-B., Johnson H.;
 RA "B cell maturation protein is a receptor for the tumor necrosis factor
 RL family member TALL-1"; Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -I- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -I- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -I- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -I- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -I- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia
 CC (T-ALL) by a chromosomal translocation t(4;16)(q26;p13), which
 CC involves TNFSF17 and IL2.
 CC -I- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; Z14954; CAA78679.1; -;
 DR EMBL; Z29575; CAA82691.1; -;
 DR EMBL; Z29574; CAA82690.1; -;
 DR EMBL; U95742; AAB67251.1; -;
 DR EMBL; AB052772; BAB60895.1; -;
 DR EMBL; AY509112; AAR84240.1; -;
 DR PIR; S43486; S43486.
 DR PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -;
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 KW 3D-structure; Chromosomal translocation; Immune response;
 KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 77 Signal-anchor for type III membrane
 FT protein (Potential).
 FT DOMAIN 78 184 Cytoplasmic (Potential).
 FT REPEAT 7 41 TNFR-Cys.
 FT SITE 3 4 Breakpoint for translocation to form
 FT IL2/TNFSF17 oncogene.
 FT DISULFID 8 21 By similarity.
 FT DISULFID 24 37 By similarity.
 FT DISULFID 28 41 By similarity.
 FT VARIANT 54 54 A -> V.
 FT VARIANT 65 65 /FTid=VAR_018755.
 FT I -> V.

RA RESULT 1
 TR17 HUMAN
 ID TR17 HUMAN STANDARD; PRT; 184 AA.
 AC Q02223;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN Name=TNFRSF17; Synonyms=BCMA, BCM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
 RP TISSUE=Lymph node, and peripheral blood leukocytes;
 RX MEDLINE=93010984; PubMed=1396583;
 RA Laabi Y., Gras M.P., Carbone P., Brouet J.C., Berger R.,
 RA Larsen C.J., Tsapis A.;
 RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
 RL by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
 RL EMBO J. 11:3897-3904(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94218235; PubMed=8165126;
 RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
 RT "The BCMA gene, preferentially expressed during B lymphoid maturation,
 RL is bidirectionally transcribed."; Nucleic Acids Res. 22:1147-1154(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99425270; PubMed=10493829;
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
 RA Fuhrmann J., Mason T., Crosby M.L., Barnshead M., Cronin L.,
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
 RT "Genome duplications and other features in 12 Mb of DNA sequence from
 RL human chromosome 16p and 16q."; Genomics 60:295-308(1999).
 RN [4]
 RN SEQUENCE FROM N.A., AND VARIANT THR-153.
 RP MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
 RA Kawasaki T., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
 RT "Presence of four major haplotypes in human BCMA gene: lack of
 RL association with systemic lupus erythematosus and rheumatoid
 RL arthritis."; Genes Immun. 2:276-279(2001).
 RN [5]
 RN SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND
 RP SER-165.
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
 RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
 RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
 RL of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
 RP MEDLINE=20363816; PubMed=10903733;
 RA Hatzoglou A., Roussel J., Bourgade M.-F., Rogier E., Madry C.,
 RA Inoue J.-I., Dovesne O., Tsapis A.;
 RT "TNF receptor family member BCMA (B cell maturation) associates with
 RL TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
 RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
 RL activated protein kinase"; J. Immunol. 165:1322-1330(2000).
 RN [7]
 RN FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,

FT VARIANT 75 75 /FTid=VAR_018756.
 FT F -> V.
 FT VARIANT 81 81 /FTid=VAR_018757.
 FT S -> N.
 FT VARIANT 153 153 /FTid=VAR_018758.
 FT A -> T.
 FT VARIANT 165 165 /FTid=VAR_012234.
 FT C -> S.
 FT /FTid=VAR_018759.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-81;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEYFDSLLHACIPQLRCSSTNPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||
 DB 1 MLQMGQCSQNEYFDSLLHACIPQLRCSSTNPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||

QY 61 GLSLIISLAVFVLMFLLRKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 DB 61 GLSLIISLAVFVLMFLLRKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||

QY 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 DB 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||

QY 181 ISAR 184
 |||||
 DB 181 ISAR 184
 |||||

RESULT 2
 Q6PE46 PRELIMINARY; PRT; 184 AA.

AC Q6PE46
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 17.
 GN Name=TNFRSP17;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 99.6%; Score 960; DB 2; Length 184;
 Best Local Similarity 99.5%; Pred. No. 3.3e-81;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEYFDSLLHACIPQLRCSSTNPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||
 DB 1 MLQMGQCSQNEYFDSLLHACIPQLRCSSTNPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||

QY 61 GLSLIISLAVFVLMFLLRKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 DB 61 GLSLIISLAVFVLMFLLRKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||

QY 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 DB 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||

QY 181 ISAR 184
 |||||
 DB 181 ISAR 184
 |||||

RESULT 3
 AAH58291 PRELIMINARY; PRT; 184 AA.

ID AAH58291
 AC AAH58291
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 17.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 99.6%; Score 960; DB 2; Length 184;

Qy 4 MAGQCSNEYDPSLLHACIPQLRCSNTPPLTCQRYCNASVTSVKTNAITWTCIGLS 63
 Db 1 MAQCQFSEYDPSLLHACKPCHLRCSN--PPATCQPCDPSVTSVKTNAITWTCIGLS 58
 Qy 64 LIISLAVFLMFLARKLSPLKDEPKFN---TCGSLGWMANIDLEKSRCTDEILPRL 119
 Db 59 LVLSLAUFTISFLURKNPEALDEPOSGQLQSGALDKADTELTIRAGDDRIFFRSL 118
 Qy 120 EYTVBECTCDCKIKPKVDSDHCFPLPAMEEGATILVTKTNDYCK-SLPAAL-SATEI 177
 Db 119 EYTVBECTCDCKIKPKVDSDHCFPLPAMEEGATILVTKTNDYCK-SLPAAL-SATEI 177
 Qy 178 EKSISAR 184
 Db 179 EKPTHTR 185

RESULT 5

T13C MOUSE STANDARD; PRT; 175 AA.

AC Q9D8D0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-
 activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor 3)
 DE (B-cell maturation defect).
 GN Name=Tnfrsf13c; Synonyms=Baffr, Bcmd, Br3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALE/C; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RT "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF";
 RL Science 293:2108-2111(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
 RC STRAIN=A/J;
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 RA Cancro M.P., Grewal I.S., Dixit V.M.;
 RT "Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency";
 RL Curr. Biol. 11:1547-1552(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schraml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,
 RA Grimmond S., Gutincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagahima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hahizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21614654; PubMed=11747827;
 RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
 RA Hilbert D.M., Hayes C.E., Cancro M.P.;
 RT "Competition for BlyS-mediated signaling through Bcmd/BR3 regulates
 RT peripheral B lymphocyte numbers";
 RL Curr. Biol. 11:1986-1989(2001).
 CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bvnt-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9D8D0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9D8D0-2; Sequence=VSP_006506;
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.
 CC -1- DISEASE: Defects in Tnfrsf13c are a cause of severe B-cell
 CC deficiency. B-cell deficient strain A/MySnJ has a 4.7 kb insertion
 CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
 CC is not detectable. B-cell lymphoplasia is normal, but the life
 CC span of peripheral B-cells is much reduced.
 CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AF373847; AAK91827.1; -;
 DR EMBL; AK008142; BAB25490.1; -;
 DR HSSP; Q96RJ3; 1QQE.
 DR MGD; MGI:1919299; Tnfrsf13c.
 KW Alternative splicing; Glycoprotein; Immune response; Receptor;
 KW Signal-anchor; Transmembrane.
 FT DOMAIN 1 71 Extracellular (Potential).
 FT TRANSMEM 72 92 Signal-anchor for type III membrane
 FT protein (Potential).
 FT DOMAIN 93 175 Cytoplasmic (Potential).
 FT REPEAT 21 38 TNFR-Cys (incomplete).
 FT DISULFID 22 35 By similarity.
 FT DISULFID 27 38 By similarity.
 FT CARBOHYD 23 23 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 133 143 Missing (in isoform 2).
 FT FTID=VSP_006506.
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
 Query Match 12.1%; Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.01;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
 Qy 7 QCSQNEYFSLHACIPCOL-----RCSNTPPLTCQRYCNASVTSVKTNAITWTCIGLS 56
 Db 21 QCNQTECFDPLRNCVSCSLFHTPTDGTHTSSLEPGTALQPGSGALRPDVALVGPALL 80

QY 57 WTCLGLSLI--ISLAVFLVFLMRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTG 111
 DB 81 GLILALTGLVGLSVLRWQQRLRTASPDTSFEGVQOE-----SLENVFPVSSET-- 129
 QY 112 EILPRGLEVTVECTEDCIKPKVDSDHCFPLPAMEGATILVTTKT 161
 DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATGLGSELVTTKT 170

RESULT 6
 Q8R4W8 PRELIMINARY; PRT; 175 AA.
 AC Q8R4W8
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE TRAF3 binding protein.
 GN Name=Trf3f3c;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizuno K., Irie S., Sato T.-A.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF350257; AAL83914.1;
 DR HSSP; Q96R33; LOOE
 DR MGQ; MGI:1919299; Tnf3rf3f3c.
 DR SQ SEQUENCE 175 AA; 18846 MW; B64EFF4B52E93B1 CRC64;

Query Match 12.1%; Score 116.5; DB 2; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.01;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSQNEYFDSLHACIPQL-----RCSNTPPLTCQRYCNASVTNSVK-----GTNAIL 56
 DB 21 QCNQTECFDLVRNCVSCLEFHTPDGTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80

QY 57 WTCLGLSLI--ISLAVFLVFLMRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTG 111
 DB 81 GLILALTGLVGLSVLRWQQRLRTASPDTSFEGVQOE-----SLENVFPVSSET-- 129

QY 112 EILPRGLEVTVECTEDCIKPKVDSDHCFPLPAMEGATILVTTKT 161
 DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATGLGSELVTTKT 170

RESULT 7
 TNR6 BOVIN STANDARD; PRT; 323 AA.
 AC P51857;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95 antigen).
 GN Name=TNFRSF6; Synonyms=AP1, FAS;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96226401; PubMed=8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.";
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic

activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC -1- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: Contains a death domain involved in the binding of FADD, and maybe to other cytosolic adaptor proteins.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; U34794; AAC48546.1; -;
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR008083; Fas_receptor.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR PRINTS; PR01680; FASRECEPTOR.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 36 Potential.
 FT CHAIN 17 323 Tumor necrosis factor receptor superfamily member 6. Extracellular (Potential).
 FT DOMAIN 17 170 Potential.
 FT TRANSMEM 171 188 Potential.
 FT DOMAIN 189 323 Cytoplasmic (Potential).
 FT REPEAT 45 80 TNFR-Cys 1.
 FT REPEAT 81 124 TNFR-Cys 2.
 FT REPEAT 125 163 TNFR-Cys 3.
 FT DOMAIN 238 306 Death.
 FT DISULFID 45 56 By similarity.
 FT DISULFID 57 70 By similarity.
 FT DISULFID 60 79 By similarity.
 FT DISULFID 82 98 By similarity.
 FT DISULFID 101 116 By similarity.
 FT DISULFID 104 124 By similarity.
 FT DISULFID 126 140 By similarity.
 FT DISULFID 143 154 By similarity.
 FT DISULFID 146 162 By similarity.
 FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
 SQ SSQUENCE 323 AA; 36445 MW; 4D8BA90E9E1F4892 CRC64;

Query Match 9.8%; Score 94; DB 1; Length 323;
 Best Local Similarity 22.1%; Pred. No. 2.3;
 Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;

QY 8 CSQ-NEYFDSLHA--CIPQL-----RCSN-----T 32
 DB 82 CSENEYTDKSHSDKRCIRCSIDEEHGLEVEQNTTRNTKCRCKSNFFCNSPCEHCN 141

QY 33 PPLTCQ-----RYCNASVTNSVKGTNA---ILWTCLGLSLIISLAVFLMFLRKISSEPL 85
 DB 142 PCTTCHGIIIEKTPTSNTKCKGRSHANLWAL-----LILLIPVLIIVKVKSRNRK 197

QY 86 KDEFKNTGSG-----LLGMANIDL-----EKSRTGD--EILPRGLEVTVECTED 130
 DB 198 KNYDCNSAASNDGRQLNTDVLGKVPISIAQOMRITEKVFVRKNGM-----EAKIDD 253

RN SEQUENCE FROM N.A.
 RP STRAIN=Stock d4-2;
 RC
 RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
 RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
 RA Cohen J., Meyer E., Sperling L.;
 RT "High coding density on the largest *Paramecium tetraurelia* somatic
 RT chromosome";
 RL Curr. Biol. 0:0-0(2004).
 RN [2]

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RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulska M.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR548612; CAH03606.1; -
SQ SEQUENCE 3005 AA, 343821 MW; D8CC6A247876A5AS CRC64;

Query Match          9.2%; Score 89; DB 2; Length 3005;
Best Local Similarity 20.3%; Pred. No. 71;
Matches 48; Conservative 26; Mismatches 59; Indels 104; Gaps 13;

QY      1 MLWAGQC-SONEYFDSLHLACIPCOLRCSSTPPLTCQ---RYC----- 41
Db       ::: ||| ::||: ||| ::||| ::||| ::||| ::||| ::|||
Db    1177 ILKVGNOCLCKGDFESSNQICQLDSC-----FTCGSSKYCIUCDPAFHLQLSNQN 1230
QY      42 -----NASVTSNKGVTNAITLCGLSLIIISLAVFVLMLFLRKLISSSPL----K 86
Db     1231 KCICDSGYYPNTS-TKQCEACNTCTKECOSVS-----QCIECPMTRYNRD 1275
QY      87 DEFANTGSGLGMANIDLEKSRTGDIBILPRGLETVTVE-----ECTCEDCTKSKPKV-- 138
Db     1276 DTFK-----CLCKDGFYEETIKMKPCPDWTCKVCQSQTCKUT 1313
QY     139 -----DSPHCFFLPAMEE--GATILVTTKTNDYCKSLPA-----ALSATEIHK 179
Db     1314 CESIHLSRFNNNSKK--PCLDGVFDVIEMQCNDKLCKTQQSIISTOCLS CVETE Q 1367

RESULT 12
Q97Db1 PRELIMINARY; PRT; 217 AA.
ID AC O97Db1
```

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT DT
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amino acid ABC transporter, permease component.
GN OrderedLocusNames=CAC3619;
OS *Clostridium acetobutylicum*.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1486;
[1]
RP
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359335; PubMed=11466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Noelling R., Lee H.M., Dubois J., Oiu D., Hitti J., Wolf Y.I.,
RA

RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium *Clostridium acetobutylicum*.";
RL J. Bacteriol. 183:4823-4838 (2001).
CC -I- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AB007858; AAK81542.1; -.
DR PIR; C97344; C97344.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.


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DR GO: 0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD.transp.
DR InterPro; IPR010065; HEQR.ABC.3TM.
DR Pfam; PF00528; BPD.transp.1; 1.
DR TIGRFAMs; TIGR01726; HEQR.perm.3TM; 1.
DR PROSITE; PS00928; ABC.TM1.1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 217 AA; 23743 MW; 36738BCD0E8A2F CRC64;

Query Match 9.2%; Score 88.5; DB 2; Length 217;
Best Local Similarity 24.8%; Pred. No. 5;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLHACIPQLRCSSNPPLTCQRYCNASV-----TNSVKGNNAI-----LWTCGLG 62
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 4 SSKLVIPVLDDGTRITLLTSCSIIGCIIGTIAMFTKTSVKVNLNLGKFTYTWILRG 63
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 63 SLIISLAVFV--LWELLRKISSPLKDEF---KNTGS-----GLGMANIDLEKSR 108
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 64 PLLQLLVYVYGFPLSDKLTWTPMKAAILGLSLNGAYIAEIRGILAIIDNGQFEAK 123
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 109 -----TGDEILPRGLETYVEEC-----TCSDCI-KSRPKVDSOH 142
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 124 ALGLTYGQTMKRIILQAIRWIPPCGNEFIAMKOTSLVSVITMBELLRKAQLLVSSG 183
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 143 CFFPLPAMEGA--TILVTTKNDYCKSLPAALSATEIEKSI 182
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 184 DAVTPYLFAGIFYLLITTIPTGIFSK-----IEKLS 215
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
Q80XB3
ID Q80XB3 PRELIMINARY; PRT; 804 AA.
AC Q80XB3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prominin-1 T2 isoform.
GN Name=Prom1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargas C.A., Huttner W.B., Corbeil D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY223521; AA072429.1; -.
DR MGD; MGI:1100886; Prom1.
DR GO; GO:0005903; C:brush border; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005902; C:microvillus; IDA.
DR InterPro; IPR008795; Prominin.
DR Pfam; PF05478; Prominin; 1.
SQ SEQUENCE 804 AA; 89983 MW; CFC9D6E8BCF9FF16 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 804;
Best Local Similarity 22.7%; Pred. No. 30;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSSNPPLTCQRYCNASVNTSVKGTNAILWTCGLSLIISLAVFLVFL 77
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 112 LVGCFECMCR-----CNK-CGGMHQKQKAPCRKCKGLSLLVLCILMSLGIIV 162
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 78 RKISSEPLKDEFKNTSGLLGMANIDLEKSRDGD-EIIL---PRGLETYVEECTCE--- 129
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 163 GFVANQOTTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 213
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 130 -----DCIKS-----KPKVDSHCPFLPAMEGATILVTK--TNDYCKSLPAL-- 172
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 214 FSDLDIGSVLGRIKDKLPKV-----TPVLEIKAWATAIKQTKDALQNMSSSLKS 266
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
Q80XB2
ID Q80XB2 PRELIMINARY; PRT; 809 AA.
AC Q80XB2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prominin-1 T3 isoform.
GN Name=Prom1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargas C.A., Huttner W.B., Corbeil D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY223522; AA072430.1; -.
DR MGD; MGI:1100886; Prom1.
DR GO; GO:0005903; C:brush border; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005902; C:microvillus; IDA.
DR InterPro; IPR008795; Prominin.
DR Pfam; PF05478; Prominin; 1.
SQ SEQUENCE 809 AA; 90605 MW; BC991E100C623AE1 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 809;
Best Local Similarity 22.7%; Pred. No. 31;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSSNPPLTCQRYCNASVNTSVKGTNAILWTCGLSLIISLAVFLVFL 77
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 117 LVGCFECMCR-----CNK-CGGMHQKQKAPCRKCKGLSLLVLCILMSLGIIV 167
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 78 RKISSEPLKDEFKNTSGLLGMANIDLEKSRDGD-EIIL---PRGLETYVEECTCE--- 129
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 168 GFVANQOTTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 218
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Y 130 -----DCIKS-----KPKVDSHCPFLPAMEGATILVTK--TNDYCKSLPAL-- 172
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 219 FSDLDIGSVLGRIKDKLPKV-----TPVLEIKAWATAIKQTKDALQNMSSSLKS 271
Q : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
Q80XB6
ID Q80XB6 PRELIMINARY; PRT; 823 AA.
AC Q80XB6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prominin T4 isoform.
GN Name=Prom1; Synonyms=Prom;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargas C.A., Huttner W.B., Corbeil D.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY099088; AAM28245.1; -.
DR MGD; MGI:1100886; Prom1.
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DR GO: GO:0005903; C:brush border; IDA.
DR GO: GO:0005887; C:integral to plasma membrane; IDA.
DR GO: GO:0005902; C:microvillus; IDA.
DR InterPro: IPR008795; Prominin.
DR Pfam: PF05478; Prominin; 1.
SQ SEQUENCE 823 AA; 92225 MW; 95F01A18DB84EFAC CRC64;

Query Match          9.0%; Score 86.5; DB 2; Length 823;
Best Local Similarity 22.7%; Pred. No. 31;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

Qy 18 LHACIPCOLRCSNTPPLTCQRYCNASVTSVKGTAAILWTCLGLSLIISLAVFVLMFL 77
Db 117 LVGCFPCMCRC-----CNK-CGGEHQRQKQNA PCRRCCLGLSLVLCILMSLGIY 167

Qy 78 RKISSEPLKDFKNTGSLGLGMANIDLEKSRTPD-EIIL---PRGLETVVECTCE---- 129
Db 168 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYNTNKKA 218

Qy 130 ----DCIKS-----KPKVSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
Db 219 FSDLDLGISVGLGRKDKLPKV-----TPVLEEIKAWATAIKQTKDALQNNSSLSKS 271

Qy 173 ---SATEIEKSISA 183
Db 272 LQDAATQTLNLTSS 285

RESULT 16
Q8CDK8 PRELIMINARY; PRT; 827 AA.
ID Q8CDK8
AC Q8CDK8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4931440N24 product:prominin, full insert sequence.
GN Name=Prom1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159;
RX Carninci P., Hayashizaki Y.; Sugahara Y., Shibata K., Itoh M.,
RX Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RN [2]
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RN [3]
RP "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159;
RX Carninci P., Hayashizaki Y.; Sugahara Y., Shibata K., Itoh M.,
RX Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RN [5]
RP "Normalization and subtraction of cap-trapper-selected cDNAs to
RP prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

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RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Kitsuunai T., Tashiro H., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Haraada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Onozaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura H., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029921; BAC26678.1; -.
DR MGD; MGI:1100886; Prom1.
DR GO: GO:0005903; C:brush border; IDA.
DR GO: GO:0005887; C:integral to plasma membrane; IDA.
DR GO: GO:0005902; C:microvillus; IDA.
DR InterPro: IPR008795; Prominin.
DR Pfam: PF05478; Prominin; 1.
SQ SEQUENCE 827 AA; 92714 MW; DBCA5ED2DF401A18 CRC64;

Query Match          9.0%; Score 86.5; DB 2; Length 827;
Best Local Similarity 22.7%; Pred. No. 31;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

Qy 18 LHACIPCOLRCSNTPPLTCQRYCNASVTSVKGTAAILWTCLGLSLIISLAVFVLMFL 77
Db 117 LVGCFPCMCRC-----CNK-CGGEHQRQKQNA PCRRCCLGLSLVLCILMSLGIY 167

Qy 78 RKISSEPLKDFKNTGSLGLGMANIDLEKSRTPD-EIIL---PRGLETVVECTCE---- 129
Db 168 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYNTNKKA 218

Qy 130 ----DCIKS-----KPKVSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
Db 219 FSDLDLGISVGLGRKDKLPKV-----TPVLEEIKAWATAIKQTKDALQNNSSLSKS 271

Qy 173 ---SATEIEKSISA 183
Db 272 LQDAATQTLNLTSS 285

RESULT 17
Q8BH12 PRELIMINARY; PRT; 834 AA.
ID Q8BH12
AC Q8BH12
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Prominin T1 isoform (Mus musculus adult male testis cDNA, RIKEN full-
DE length enriched library, clone:4932416E19 product:prominin, full
DE insert sequence).
GN Name=Prom1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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SQ SEQUENCE 842 AA; 94478 MW; 734C10D715B5BC92 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 842;
 Best Local Similarity 22.7%; Pred. No. 32;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQOLRCSSNTPLTQRYCNASVSKGTNAILMTCLGLSLIISLAVFLMFL 77
 DB 126 LVGCFPCMCRC-----CNK-CGEMHQKQKQAPCRRKCLGLSLVCLLMSLGIY 176

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSTGD-EIIL---PRGLETYVECTCE--- 129
 DB 177 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTTNKKA 227

QY 130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTK-TNDYCKSLPAAL-- 172
 DB 228 FSDLDGIGSVLGRKIDQLKPKV-----TPVLEIKAMATAIKQTKDALQNMSSLSKS 280

QY 173 ---SATEIEKSISA 183
 DB 281 LQDAATQTLNLTSS 294

RESULT 19

FWL1 MOUSE

AC 054990; 035408; STANDARD; PRT; 867 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Prominin 1 precursor (Prominin-like protein 1) (Antigen AC133 homolog).

GN Name=Prom1; Synonym=Prom11, Prom;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Miraglia S., Godfrey W., Buck D.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=98024147; PubMed=9356465;

RA Weigmann A., Corbell D., Helliwig A., Huttner W.B.;

RT "Prominin, a novel microvilli-specific polytopic membrane protein of the apical surface of epithelial cells, is targeted to plasmalemmal protrusions of non-epithelial cells.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430(1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: In the embryo, expressed on the apical side of neuroepithelial cells and of other epithelia such as lung buds, gut and ureter buds. In the adult, expressed at the apical side of the kidney tubules and of the ependymal layer of the brain. Not expressed in gut, liver, lung, pituitary, adrenal, heart or spleen.

CC -1- SIMILARITY: Belongs to the prominin family.

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CC -----

DR EMBL; AF039663; AAB96916.1; -

DR EMBL; AF026269; AAB86715.1; -

DR PIR; T08881; T08881.

DR MGD; MGI:1100886; Prom1.

DR GO; GO:0005903; C:brush border; IDA.

DR GO; GO:0005887; C:integral to plasma membrane; IDA.

DR GO; GO:0005902; C:microvillus; IDA.

DR InterPro; IPR008795; Prominin.

DR Pfam; PF05478; Prominin; 1.

KW Glycoprotein; Signal; Transmembrane.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 867 Prominin 1.

FT DOMAIN 20 107 Extracellular (Potential).

FT TRANSMEM 108 128 Potential.

FT DOMAIN 129 158 Cytoplasmic (Potential).

FT TRANSMEM 159 179 Potential.

FT DOMAIN 180 434 Extracellular (Potential).

FT TRANSMEM 435 455 Potential.

FT DOMAIN 456 487 Cytoplasmic (Potential).

FT TRANSMEM 488 508 Extracellular (Potential).

FT DOMAIN 509 794 Potential.

FT TRANSMEM 795 815 Potential.

FT DOMAIN 816 867 Cytoplasmic (Potential).

FT CARBOHYD 273 273 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 291 291 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 332 332 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 374 374 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 415 415 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 554 554 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 581 581 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 732 732 N-linked (GlcNAc. .) (Potential).

FT CONFLICT 64 64 S -> N (in Ref. 2).

FT CONFLICT 84 84 K -> N (in Ref. 2).

FT CONFLICT 94 102 Missing (in Ref. 2).

FT CONFLICT 668 668 P -> L (in Ref. 2).

FT CONFLICT 844 844 G -> D (in Ref. 2).

SQ SEQUENCE 867 AA; 97112 MW; D442F6372525B3C8 CRC64;

Query Match 9.0%; Score 86.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 33;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQOLRCSSNTPLTQRYCNASVSKGTNAILMTCLGLSLIISLAVFLMFL 77
 DB 126 LVGCFPCMCRC-----CNK-CGEMHQKQKQAPCRRKCLGLSLVCLLMSLGIY 176

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSTGD-EIIL---PRGLETYVECTCE--- 129
 DB 177 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTTNKKA 227

QY 130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTK-TNDYCKSLPAAL-- 172
 DB 228 FSDLDGIGSVLGRKIDQLKPKV-----TPVLEIKAMATAIKQTKDALQNMSSLSKS 280

QY 173 ---SATEIEKSISA 183
 DB 281 LQDAATQTLNLTSS 294

RESULT 20

Q6CCL1

ID Q6CCL1 PRELIMINARY; PRT; 1309 AA.

AC Q6CCL1;

DT 01-OCT-2004 (Created)

DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Similar to sp|P08640 Saccharomyces cerevisiae YIR019c STAL extracellular alpha-1.

GN ORFNames=VALI0C08473g;

OS Yarrowia lipolytica (Candida lipolytica).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI_TaxID=4952;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RG GENOLEVURES;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anchouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisramé A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrast A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicraud J.M., Nikolski M., Oztas S., Oxier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 SQ EMBL; CR382129; CAG81904.1; -;
 SQ SEQUENCE 1309 AA; 137079 MW; 7D2E2927115D6CC2 CRC64;

Query Match 8.9%; Score 86; DB 2; Length 1309;
 Best Local Similarity 24.0%; Pred. No. 56;
 Matches 52; Conservative 17; Mismatches 78; Indels 70; Gaps 11;
 DB 21 CIPCOLRCSNTPPLTCQRYCNAS-----VTNSVKGNTNAILWT---CLGLSLIISLA 69
 DB 813 CLETVVASISGPTTVINNICTTSAPVPCLEVTASVSGSTIVINDICKTVDPCITTE 872

QY 70 VFVLMFLRKISSEP---LKDFPKNTGSGLLGMANIDLE---KSRGTD-----E 112
 DB 873 VVT-----VSGTPATMKDKVQCQTADPCLETAIVTLGTPATVTKDICTSADPCVETE 925

QY 113 ILPRGLETVBECTCEDCKSPKVD-----SDHCFPLPAMEEGAT 154
 DB 926 VTVVSGTSTV---TKNSCITSTPVADPCVVTETISSGTTITEVTRDICTPAPTVPVVTST 982

QY 155 ILV---TTKT-----NDYCKNSLPA-----ALSATEI 177
 DB 983 VTVPATITKTITVCEBEVCTTIPVTLTALVLTSTTEI 1019

RESULT 21
 QY1X8
 ID QY1X8 PRELIMINARY; PRT; 1193 AA.
 AC QY1X8;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Protein tyrosine kinase.
 GN Name=EFTK178;
 OS Ephydatia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haploclerida; Spongillidae; Ephydatia.
 OX NCBI_TaxID=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99246375; PubMed=10229568;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 RA Miyata T.;
 RT "Extensive gene duplication in the early evolution of animals before
 the parazoan-eumetazoan split demonstrated by G proteins and protein
 tyrosine kinases from sponge and hydra.";
 RL J. Mol. Evol. 48:646-653(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21601119; PubMed=11738833;
 RA Suga H., Katoh K., Miyata T.;
 RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
 domain shufflings in the early evolution of animals before the
 parazoan-eumetazoan split.";

RL Gene 280:195-201(2001).
 DR EMBL; AB006570; BAA81724.2; -;
 DR HSSB; P08069; LJQH.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
 DR GO; GO:0015740; F:transferase activity; IEA.
 DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00261; FU; 6.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00552; TNFR_NGFR_1; UNKNOWN 1.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;

Query Match 8.9%; Score 85.5; DB 2; Length 1193;
 Best Local Similarity 22.3%; Pred. No. 57;
 Matches 37; Conservative 28; Mismatches 56; Indels 45; Gaps 8;
 QY 2 LQWAGCQSNQYFDSLLHACIPCOLRCSNTPP-----LTCQRYCNASVTNSVKGNTNAIL 56
 DB 715 LCVSGCSNDTEYQDAALN-CLPCAAGCIGCSGPSISQCLTCA--SGSCTTTDVQSSGGII 771

QY 57 WTCLGLSLIISLA---VFVLMFLRKISSEPKDFKNTGSGLLGMANIDLEKSRGTDEI 113
 DB 772 GIVFGSIVVIFLATSIVLLIFIVRYEHKVPKNTQSTA---MCYSN-----GNET 820

QY 114 ILPRGLETVBECTCEDCKSPKVDSDH-----CPPLPAMEEGATI 155
 DB 821 LRP-----PKLPPDATRLIITPETALEQCVL 847

RESULT 22
 QY1X8
 ID QY1X8 PRELIMINARY; PRT; 938 AA.
 AC QY1X8;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein At3g48195.
 GN Name=At3g48195;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY091078; AAM13898.1; -.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001683; PX.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS0195; PX; 1.
DR PROSITE; PS0195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 938 AA; 103602 MW; 3E78395D65D75C95 CRC64;

Query Match      8.7%; Score 83.5; DB 2; Length 938;
Best Local Similarity 29.4%; Pred. No. 68;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGNTNAILWTCLGLSLIISLAVFVLMFLRLKTSSEPLKD-EFKN--TGS 94
Db 29 ERYCSA---NSALGTFSM---C-----SSTGFFQDSEFENFSLGP 62
Qy 95 GLGGMANIDLEKSGRTGDEIILPRGLETVTEECTCICKP-----KVDSHCFPLPAM 149
Db 63 SLVKLSLDM--SRLGD-----RGIHFDEGSGCNGRSSSAPGLNTGNVNDMCGDL--M 113
Qy 150 EEGATI 155
Db 114 DGGATI 119

RESULT 23
Q9STR8 PRELIMINARY; PRT; 1998 AA.
AC Q9STR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T24C20_80.
GN Names=T24C20_80;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN SEQUENCE FROM N.A.
RA Choise N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Queirer F., Salanoubat M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096856; CAB51067.1; -.
DR PIR; T13009; T13009.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS0195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 1998 AA; 223512 MW; 8B3D6A03CD248F55 CRC64;

Query Match      8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 1.5e+02;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGNTNAILWTCLGLSLIISLAVFVLMFLRLKTSSEPLKD-EFKN--TGS 94
Db 1089 ERYCSA---NSALGTFSM---C-----SSTGFFQDSEFENFSLGP 1122
Qy 95 GLGGMANIDLEKSGRTGDEIILPRGLETVTEECTCICKP-----KVDSHCFPLPAM 149
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Db 1123 SLVKLSLDM--SRLGD-----RGIHFDEGSGCNGRSSSAPGLNTGNVNDMCGDL--M 1173
Qy 150 EEGATI 155
Db 1174 DGGATI 1179

RESULT 24
Q8C6R5 PRELIMINARY; PRT; 449 AA.
AC Q8C6R5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230011u17 product:protein tyrosine kinase 2 beta, full insert sequence. (fragment).
GN Names=Ptk2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[1]
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530913; PubMed=11076861;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK054002; BAC35615.1; -.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0004672; F:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR SMART; SM00295; B41; 1.
DR KINASE; PS50057; FERM_3; 1.
FT NON TER 449 449
SQ SEQUENCE 449 AA; 51577 MW; D3565BCBA7D32B84 CRC64;

Query Match 8.6%; Score 83; DB 2; Length 449;
Best Local Similarity 26.9%; Pred. No. 35;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLTYVECTCEDCIKPKV 138
Db 249 KPFNT---LAGFANIDQETVRCLEIQGNWITVDLVIGPKGIQRLTSDTKPTCLAEFKQI 305

QY 139 DSDHCPPLPAME-----EGATILVTTKND-----YCK 166
Db 306 KSTRCLPLEETQAVLQIGIEGAPQSLSIKTSLSAEANMADLDGYCR 353

RESULT 25
Q8C9L4 PRELIMINARY; PRT; 474 AA.
AC Q8C9L4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630043J01 product:protein tyrosine kinase 2 beta, full
DE insert sequence.
GN Names=Ptk2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";

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RL Nature 420:563-573(2002).
[4]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK041878; BAC31090.1; -.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0004672; F:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR SMART; SM00295; B41; 1.
DR KINASE; PS50057; FERM_3; 1.
SQ SEQUENCE 474 AA; 54201 MW; A1A83BCB191B55FB CRC64;

Query Match 8.6%; Score 83; DB 2; Length 474;
Best Local Similarity 26.9%; Pred. No. 37;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLTYVECTCEDCIKPKV 138
Db 249 KPFNT---LAGFANIDQETVRCLEIQGNWITVDLVIGPKGIQRLTSDTKPTCLAEFKQI 305

QY 139 DSDHCPPLPAME-----EGATILVTTKND-----YCK 166
Db 306 KSTRCLPLEETQAVLQIGIEGAPQSLSIKTSLSAEANMADLDGYCR 353

RESULT 26
Q7RAA5 PRELIMINARY; PRT; 164 AA.
ID Q7RAA5;
AC Q7RAA5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DHHC zinc finger domain, putative.

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Query Match 8.5%; Score 82; DB 2; Length 327;
Best Local Similarity 23.0%; Pred. No. 31;
Matches 54; Conservative 25; Mismatches 68; Indels 88; Gaps 15;

QY 8 CSQ-NEVFDLLHA--CIPCOL-----RCSN-----T 32
 DB 84 CSENEYTDKSHSDKIRCSVDEEHGLEVEHNCTRTONTKCRCKSNFFCNSPCEHCN 143
 QY 33 PPLTCO---RYCNASVTNSVKG---TNAIWTCLGLSLIISLAVFLMLRK----- 79
 DB 144 PCTTCEHGIIEKTPNTSKCRSRHTNS-LWALLILLGLLILFLIYKVRRRNRKK 202
 QY 80 ---ISSEPLKDFKNTGSGLLGMANIDLEKSRG-----DEIILPRGLEVTVEEC 126
 DB 203 NGNCVSAASDEGRQ-----LNLTDVLDGKYIPSIABLMIKTEVKEFVRKNGM-----EEA 253
 QY 127 TCSDCTKSQKPVSDHCFFPLPAMEGATIL-----VTTKNDYV-----KSLPAALS 173
 DB 254 KIDDIIMH-----DNLH-----ETAQKQVLLRKRYQSHGKNAYCTLTKNLPKALA 299

RESULT 29
 Q8C2G0 PRELIMINARY; PRT; 967 AA.
 AC Q8C2G0
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:B430023005 product:protein tyrosine kinase 2 beta, full insert sequence.
 DE Name=Ptk2b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Tagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T., RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK08696; BAC40510.1; -
 DR HSSP; Q05397; 1K04.
 DR MGD; MGI:104908; Ptk2b.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004672; P:protein kinase activity; IDA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro; IPR000239; Band 4.1.
 DR InterPro; IPR009065; FERM.
 DR InterPro; IPR005189; Focal AT.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR007119; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF03623; Focal AT; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; TyRK; 1.
 DR PROSITE; PS00057; FERM 3; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN 1.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 967 AA; 111131 MW; D65A8C83847BA62F CRC64;

Query Match 8.5%; Score 82; DB 2; Length 967;
 Best Local Similarity 26.9%; Pred.No. 97;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEVTVEECTCDICKSPKV 138
 DB 249 KKFNT---LAGFANIDQETVRCLEIQQWITVDLVIGPKGIRQLTSDIKPTCLAEFKQI 305
 QY 139 DSDHCFFLPAME-----EGATILVTTKND-----YCK 166
 DB 306 RSIRCLPLEETOAVLQLGIEGAPQSLSIKTSSLAEEANMADLIDGYCR 353

RESULT 30
 FAK2_MOUSE
 ID FAK2_MOUSE STANDARD; PRT; 1009 AA.
 AC Q9QVE9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (PAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related adhesion focal tyrosine kinase).
 DE Name=Ptk2b; Synonyms=FAK2, PYK2, Raftek;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RA "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain.";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [2]
 RP PTNS1 BINDING.
 RX MEDLINE=99401000; PubMed=10469599;
 RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
 RA Schraven B., Neel B.G.;
 RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
 RT multi-protein complexes in macrophages.";
 RL Curr. Biol. 9:927-930(1999).
 RN [3]
 RP PHOSPHORYLATION SITES TYR-402; TYR-580 AND TYR-881.
 RX MEDLINE=21313779; PubMed=11420674; DOI=10.1038/sj/onc/1204359;
 RA Nakamura K., Yano H., Schaefer E., Sabe H.;
 RT "Different modes and qualities of tyrosine phosphorylation of Pak and
 RT Pyk2 during epithelial-mesenchymal transdifferentiation and cell
 RT migration: analysis of specific phosphorylation events using site-
 RT directed antibodies.";
 RL Oncogene 20:2626-2635(2001).
 RN [4]
 RP PHOSPHORYLATION SITE TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RX MEDLINE=21396597; PubMed=11493697; DOI=10.1073/pnas.171269898;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Binds DBP2 (By similarity). Interacts with Crk-
 CC associated substrate (Cas), PTNS1, Nephrocystin and OPHN1L.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase.
 CC -1- PTM: Phosphorylated on tyrosine residues in response to various
 CC stimuli that elevate the intracellular calcium concentration, as
 CC well as by PKC activation. Recruitment by Nephrocystin to cell
 CC matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 DR HGSP; Q05397; IK04.
 DR IntAct; Q9QVP9; -.
 DR MGD; MGI:104908; Ptk2b.
 DR InterPro; IPR000299; Band 4.1.
 DR InterPro; IPR009065; FERM¹
 DR InterPro; IPR005189; Focal AT.
 DR InterPro; IPR011009; Kinase¹-like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr.pkinase.
 DR InterPro; IPR008266; Tyr.pkinase_AS.
 DR Pfam; PF031623; Focal AT; 1.
 DR Pfam; PF000659; Pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; TykKc; 1.
 DR PROSITE; PS00660; FERM 1; FALSE NEG.
 DR PROSITE; PS00661; FERM 2; FALSE NEG.
 DR PROSITE; PS00057; FERM 3; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Phosphorylation; transferase; Tyrosine-protein kinase.
 FT DOMAIN 39 359 FERM.
 FT DOMAIN 425 683 Protein kinase.
 FT NP_BIND 431 439 ATP (By similarity).
 FT BINDING 457 457 ATP (By similarity).
 FT ACT_SITE 549 549 Proton acceptor (By similarity).
 FT DOMAIN 701 767 Pro-rich.
 FT DOMAIN 831 869 Pro-rich.
 FT DOMAIN 868 1009 Focal adhesion targeting (FAT).
 FT MOD_RES 402 402 Phosphotyrosine.
 FT MOD_RES 579 579 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 580 580 Phosphotyrosine.
 FT MOD_RES 881 881 Phosphotyrosine.
 SQ SEQUENCE 1009 AA; 115821 MW; 963959FF56DF9605 CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 1e+02;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLYTVBECTCDCKSPKV 138
 Db 249 KPFTN---LAGFANIDQETVRCLEIQGWNITVDLVIGPKGIRQLTSQDKPTCLAEFKQI 305
 QY 139 DSDHCPLPAME-----EGATILVTXTND-----YCK 166
 Db 306 RSTRCLPLEETQAVLQLGIEGAPQSLSIKTSLSLAENMADLIDGYCR 353
 RESULT 31
 ID_FAK2_RAT STANDARD; PRT; 1009 AA.
 AC P70600; O88489; Q63201;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 DE 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 DE beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN Names=Ptk2b; Synonyms=Fak2, Pyk2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RA Wilms M., Anderregg R.J., Graves L.M., Earp H.S.;
 RT "Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 RL J. Biol. Chem. 271:29993-29998(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95403356; PubMed=7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobitoka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).

[3]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
DOMAIN.
TISSUE=Hippocampus;
MEDLINE=98311659; PubMed=9645946;
Xiong W.-C., Macklem M., Parsons J.T.,
"Expression and characterization of splice variants of PYK2, a focal
adhesion kinase-related protein.";
J. Cell Sci. 111:1981-1991(1998).
-!- FUNCTION: Involved in calcium induced regulation of ion channel
and activation of the map kinase signaling pathway. May represent
an important signaling intermediate between neuropeptide activated
receptors or neurotransmitters that increase calcium flux and the
downstream signals that regulate neuronal activity. Interacts with
the SH2 domain of Grb2. May phosphorylate the voltage-gated
potassium channel protein Kv1.2. Its activation is highly
correlated with the stimulation of c-Jun N-terminal kinase
activity.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-!- SUBUNIT: Interacts with PTPNS1 and DDEF2 (By similarity). Isoform
1, but not isoform 2, interacts with Crk-associated substrate
(Cas), Nephrocystin and OPHNL.
-!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
induces the membrane-association of the kinase (By similarity).
Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1;
IsoId=P70600-1; Sequence=Displayed;
Name=2; Synonyms=PRNK;
IsoId=P70600-2; Sequence=VSP_004982, VSP_004983;
Name=3; Synonyms=PYK2s;
IsoId=P70600-3; Sequence=VSP_004984;
-!- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
in the spleen and other tissues, whereas isoforms 2 and 3 are
expressed in the spleen and brain (highest in cerebellum).
-!- PTM: Phosphorylated on tyrosine residues in response to various
stimuli that elevate the intracellular calcium concentration, as
well as by PKC activation. Recruitment by Nephrocystin to cell
matrix adhesions initiates Tyr-402 phosphorylation (By
similarity). In monocytes, adherence to substrata is required for
tyrosine phosphorylation and kinase activation. Angiotensin II,
thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
autophosphorylation and increase kinase activity.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
subfamily.
-!- SIMILARITY: Contains 1 FERM domain.

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or send an email to license@isb-sib.ch).

EMBL; U69109; AAC52895.1; -;
EMBL; D45854; BAA02290.1; -;
EMBL; AF063890; AAC28340.1; -;
FIR; A57434; A57434.
HSSP; Q05397; 1K04.
RGD; 628758; Ptk2b.
InterPro; IPR000299; Band 4.1.
InterPro; IPR009085; FERM.
InterPro; IPR005189; Focal_At.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF03623; Focal_At; 1.
Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS00557; FERM_3; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_TYR; 1.
KW Alternative splicing; ATP-binding; Direct protein sequencing;
KW Phosphorylation; Transferase; Tyrosine-protein kinase.
FT DOMAIN 39 359
FT DOMAIN 425 683 Protein kinase.
FT NP_BIND 431 439 ATP (By similarity).
FT BINDING 457 457 ATP (By similarity).
FT ACT_SITE 549 549 Proton acceptor (By similarity).
FT DOMAIN 701 767 Pro-rich.
FT DOMAIN 831 869 Pro-rich.
FT DOMAIN 868 1009 Focal adhesion targeting (FAT).
FT MOD_RES 402 402 Phosphotyrosine (By similarity).
FT MOD_RES 579 579 Phosphotyrosine (by autocatalysis) (By
similarity).
FT MOD_RES 580 580 Phosphotyrosine (By similarity).
FT MOD_RES 881 881 Phosphotyrosine (By similarity).
FT VARSPPLIC 1 771 Missing (in isoform 2).
FT VARSPPLIC 772 780 NVPKRHSMR -> MGLIVLSSQ (in isoform 2).
FT VARSPPLIC 739 780 Missing (in isoform 3).
FT CONFLICT 205 205 E -> A (in Ref. 2).
FT CONFLICT 807 807 V -> F (in Ref. 3).
SQ SEQUENCE 1009 AA; 115784 MW; D435A475BCA49E9B CRC64;

Query Match 8.5%; Score 82; DB 1; Length 1009;
Best Local Similarity 26.9%; Pred. No. 1e+02;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSLGGMANIDLEKSR-----TGDEILPRGLVTECTEDCIKSKPKV 138
Db 249 KFNPT---LAGFANIDQETRYCELIGQWNTVDLVIGPKGIRQLTSQDKPTCLAEFKQI 305

QY 139 DSDHCPLPAME-----EGATILVTTKND-----YCK 166
Db 306 RSIRCLPLEBTQAVLQLGIEGAPQSLSIKTSLSLAENMADLIDGYCR 353

RESULT 32
Q8VEV6 PRELIMINARY; PRT; 314 AA.
AC Q8VEV6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Olfactory receptor MOR202-36 (Olfactory receptor Olfr1475).
GN Name=Olfr1475;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory

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receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
RL Genome Biol. 4:R71-R71(2003).
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073792; AAL61455.1; -
DR EMBL; AY318694; AAP71836.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR InterPro; IPR00725; Olfact_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 34996 MW; 9C7B11A5917EA632 CRC64;

Query Match 8.5%; Score 81.5; DB 2; Length 314;
Best Local Similarity 30.4%; Pred. No. 33;
Matches 31; Conservative 16; Mismatches 40; Indels 15; Gaps 6;

Qy 8 CSQNEYFDSLHACIP-CQLRCSNT-----PPLTCQRYCNASVTNSVKGTNAILWT 58
Db 146 CYMGILQSIHVALACFLSCNSVINHFCDIPPL-LDISCDYTNIEI--TVLILGT 202

Qy 59 CLG-LSLIISLAVFLVMP--LLRKISSEPLKDFKNTGSGLL 97
Db 203 CDGILTLVILNTYLLIFIALIRMSAEAKAFSTCASHLI 244

RESULT 33
Q94711 ID Q94711 PRELIMINARY; PRT; 2233 AA.
AC Q94711;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S1C surface protein.
OS Paramacium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramacium.
OC NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92106337; PubMed=1762150;
RA Nielsen E., You Y., Forney J.;
RT "Cysteine residue periodicity is a conserved structural feature of
variable surface proteins from Paramacium tetraurelia.";
RL J. Mol. Biol. 222:835-841(1991).
DR EMBL; M65164; AAA61740.1; -
DR PIR; T28669; T28669.
DR InterPro; IPR002895; Paramacium SA.
DR Pfam; PF01508; Paramacium SA; 25.
DR SMART; SM00639; PSA; 26.
SQ SEQUENCE 2233 AA; 237076 MW; C064FE0AF7BB873B CRC64;

Query Match 8.4%; Score 81; DB 2; Length 595;
Best Local Similarity 24.5%; Pred. No. 72;
Matches 39; Conservative 27; Mismatches 49; Indels 44; Gaps 10;

Qy 6 GCSQNEYFDSLHACIP-CQLRCSNTTTPPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL 64
Db 520 GSCVQKQ-----CSAASQDNTHAQCOEYLPACTLSNTKG-----CIDLPL 561
Qy 65 IISLAVFLVFLRKISSEPLKDFKNTGSGLLGMANIDL-----EKSRTGDEILLRGL 120
Db 562 TCSEA-----LVKENCCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-----D 603
Qy 121 YTVVEECTC---EDCTKSKPKVDSHCFPLPAMEEGATI-----LVTTKTN 162
Db 604 YTVELCEAYKPSNSCV---PNGTKKGMELAAKCESRTIKEQCDVAGTKTN 651

RESULT 34
Q39191 ID Q39191 PRELIMINARY; PRT; 595 AA.
AC Q39191;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine threonine kinase.
GN Name:pro25;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=93066369; PubMed=1438303;
RA Smith T.A., Kohorn B.D.;
RT "An Arabidopsis serine threonine kinase homologue with an EGF repeat
selected in yeast for its specificity for a thylakoid membrane
protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L04999; AA32844.1; -
DR HSP; P01130; 1H28.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; EGF-like domain; Kinase; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 595 AA; 65898 MW; 7B58FCA656E0641 CRC64;

Query Match 8.4%; Score 81; DB 2; Length 595;
Best Local Similarity 24.5%; Pred. No. 72;
Matches 39; Conservative 27; Mismatches 49; Indels 44; Gaps 10;

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	Query Match	8.4%;	Score 81;	DB 2;	Length 773;	
	Best Local Similarity	21.7%;	Pred. No. 95;			
	Matches 40;	Conservative 25;	Mismatches 91;	Indels 28;	Gaps 6;	
Qy	23	PCQLRCSSNPPLTCQ-----RYCN-----ASVTNSVKGNTNAILWTCL---	GLSL	64		
	:	:	:	:	:	:
Db	184	PPKSNATCQGPCKSCDPVHDIRISITGYCNNRGKPTQANSVTAIRLLGTTSTYDGLQA	243			
Qy	65	IISIAFVLMLPRLKRISSEPKLDFKNKTG-SGLLGMANIDLEKSRGTGDEIILPRGLETVT	123			
	:	:	:	:	:	:
Db	244	IRNTSVTGSPLPSPRLISNKLHDGGSTPNFGSPNVNHLHMOTGFQIAHDIIFMPSSAKDG	303			

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Qy 124 EECTCECICSKPKVDSDHCHCPPLPAMEGAILVTTKNTDCKSLPAAUSA-----TE 175
Db 304 SSLNCTSC--SSPTTITNCAPIAPAPADDKYFTVPVSRTEARCIRLTRALNGOSGFGVRTQ 361

Qy 177 IEKS 180
Db 362 IDQN 365

RESULT 36
Q7TQO9 ID TQO9 PRELIMINARY; PRT; 314 AA.
AC Q7TQO9,
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OFactory receptor Olfz1472.
GN Name=Olfz1472;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels.";
RL Genome Biol. 4:R71-R71(2003).
[2]
RN SEQUENCE FROM N.A.
RP Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY318691; AAP71834.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO: InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35001 MW; DF19DD0033F8B2FD8 CRC64;

Query Match 8.4%; Score 80.5; DB 2; Length 314;
Best Local Similarity 30.4%; Pred. No. 41;
Matches 31; Conservative 16; Mismatches 40; Indels 15; Gaps 6

Qy 8 CSONEYFDSLHACIP-CQLRCSNT-----PPLTCQRYCNASVTNSVKGTTAILWT 58
Db 146 CYMGILQSSITHVALAFCLSPCNSNVINHFPCDIPPL-LEISCSDTYTNEI--TVLILGT 202

Qy 59 CLG-LSLIISLAVFLMF--LLRKISSEPLKDFKNTGSGLL 97
Db 203 CDGILTULVILTYLLIFAILRMRSVEAQRKAFSTCASHLI 244

RESULT 37
Q8IN99 ID Q8IN99 PRELIMINARY; PRT; 487 AA.
AC Q8IN99;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG31262-PA.
GN ORFNames=CG31262;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```

OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Buser D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nueskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Science 287:2185-2195(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426065; PubMed=12537568;
 RX Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Science 287:2185-2195(2000).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RX Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.I., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 [5]
 RN SEQUENCE FROM N.A.
 RP FLYBASE;
 RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RP FLYBASE;
 RG Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003716; AN13739.1; -;
 DR FLYBase; FBgn0051262; CG31262.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001734; Na/solut_symp; 1.
 DR PROSITE; PS50283; NA SOLUT_SYMP 3; 1.
 SQ SEQUENCE 487 AA; 53156 MW; 45481312B8CC2C9C CRC64;
 Query Match 8.4%; Score 80.5; DB 2; Length 487;
 Best Local Similarity 23.7%; Pred. No. 65;
 Matches 42; Conservative 28; Mismatches 60; Indels 47; Gaps 8;
 QY 48 SVKGTNAILWTCLGLSLIISLAVFVLMFLLR-----KISSEPLKDEF----- 89
 Db 311 SERQSTILLIKTCI---IFQILAFILVFLLOHLRGILSVCSISSITAGTSGVFTLGLML 367
 QY 90 ---KNT-GSGLIGMANIDLEK-SRTGDEILPRG-----LEYVTECTCEDCIKSPKV 138
 Db 368 FPMANTIGTAGVGLSVLLAGWISFGSIAAASQGLKSGMLPVSVEKCVGNVTLPEDPWV 427
 QY 139 DSPHCPL-----PMEEGATILVTTKNDYCKSLPALSALETEKSI 181
 Db 428 DQDQVFLYRLSVHVVWSPIGWTVAVVGVGLVSLITKPAD-IKTLHAELISPVHRSV 483
 RESULT 38
 ID 081820 PRELIMINARY; PRT; 735 AA.
 AC 081820;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Wall-associated kinase 1 (Hypothetical protein Atlg21250).
 GN Name=waki; Synonyms=Atlg21250;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99308512; PubMed=10380805;
 RA He Z.H., Cheeseman I., He D., Kohorn B.D.;
 RT "A cluster of five cell wall associated receptor kinase genes, Waki-5,
 RT are expressed in specific organs of Arabidopsis."
 RL Plant Mol. Biol. 39:1189-1196(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,

RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ikehida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AJ006956; CA008794.1; -.
DR EMBL: AY039917; AAK64021.1; -.
DR EMBL: BT001967; AAN71966.1; -.
DR HSSP: P01130; 1H28.
DR GO: GO:0005524; F-ATP binding; IEA.
DR GO: GO:0005509; P:calcium ion binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000152; ASx hydroxyl_S.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF07645; EGF_CA; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00179; EGF_CA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00026; EGF_2; 1.
DR PROSITE: PS01187; EGF_3; 2.
DR PROSITE: PS01187; EGF_CA; UNKNOWN 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; EGF-like domain; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 735 AA; 81210 MW; AAD41A28296093B6 CRC64;

Query Match 8.3%; Score 80; DB 2; Length 735;
Best Local Similarity 24.2%; Pred. No. 1.1e+02;
Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps 10;

QY 8 CSONEYFDSLHACIPCO-----LRCSN-----TPPLTCOR-----YQNA-----SV 45
DB 264 CRNCEGFGNYPYLSAGCDVNECTSTHRCNSDPKTRNKVGFGYCKQSGYRLDT 323
QY 46 TNSVK-----GTNAIWLTCGLSLIISLAVFLMLKISSPLKDE-FKNTGSGLL-- 97
DB 324 TMSCKRKEFAWTTILLVTTIGF-LVILGVACIQQRMKHLKDTKLRQEPQNGGGMATQ 382

QY 98 -----GMANID-----LEKSRG--DEIILPRGLEVTYV 123
DB 383 RLSGAGPSNVVDVKIFTEGDMKATNGVAESRIILGQGGQGV 423

RESULT 39
Q8KLY1
ID Q8KLY1 PRELIMINARY; PRT; 153 AA.
AC Q8KLY1; 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A15101;
RX MEDLINE=22787088; PubMed=12904565;
RA Desnoes N., Lin M., Guo X., Ma L., Carreno-Lopez R., Elmerich C.;
RT "Nitrogen fixation genetics and regulation in a Pseudomonas stutzeri
RL strain associated with rice.";
Microbiology 149:2251-2262(2003).

DR EMBL: AJ297529; CAD44480.1; -.
DR GO: GO:001846; F:carbon-sulfur lyase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR006913; GFA.
DR Pfam: PF04828; DUF636; 1.
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17188 MW; 0C849770A6EEA7C7 CRC64;

Query Match 8.2%; Score 79.5; DB 2; Length 153;
Best Local Similarity 32.9%; Pred. No. 24;
Matches 27; Conservative 7; Mismatches 35; Indels 13; Gaps 2;

QY 110 GBEIILPRGLEVTVECTCEDCIKPKVDSDHCFPLPAMEGATILVTKTNDY----- 164
DB 34 GDVIRVAGSRPYRVGLCHLDCRKHGAL-----PHASAIFPQTAVTVTGETRDYAGRF 88
QY 165 ---CKSLPAALGATEIEKSISA 183
DB 89 CPGSGSVFARTADELEVSIGA 110

RESULT 40
ID_FAK2_HUMAN STANDARD; PRT; 1009 AA.
AC Q14289; Q13475; Q14290; Q16709;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
DE 2) (PAK2) (Prolin-rich tyrosine kinase 2) (Cell adhesion kinase
DE beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
DE adhesion focal tyrosine kinase).
DE Homo sapiens (Human).
GN Names=PTK2B; Synonyms=FAK2, PYK2, RAFTK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95379967; PubMed=7544443;
RA Lev S., Moreno H., Martinez R., Canoll P., Peles E., Musacchio J.M.,
RA Florman G.D., Rudy B., Schlessinger J.;
RT "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of
RT ion channel and MAP kinase functions.";
RL Nature 376:737-745(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=96435932; PubMed=8838818;
RA Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
RT "Molecular cloning and assignment of PAK2, a novel human focal
RT adhesion kinase, to 8p11.2-p22 by nonisotopic in situ hybridization.";
RL Genomics 32:484-486(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=95403356; PubMed=7673154;
RA Sasaki H., Nagura K., Ichino M., Tobiooka H., Kotani K., Sasaki T.;
RT "Cloning and characterization of cell adhesion kinase beta, a novel
RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
RL J. Biol. Chem. 270:21206-21219(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96070905; PubMed=7499242;
RA Abraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
RA Fasztor L.M., White R.A., Groopman J.E., Avraham H.;
RT "Identification and characterization of a novel related adhesion focal
RT tyrosine kinase (RAFTK) from megakaryocytes and brain.";
RL J. Biol. Chem. 270:27742-27751(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Monocytes;

[illegible]

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QY 88 EFKNTGSLGLGMANIDLEKSR-----TCDEIILPRGLETVVEECTCDDCIKSKPKV 138
Db 249 KFFNT---LAGFANIDQTYRCLELIQGNWITVDLVIGPKGIQRLTSQDAKPTCLAEFKQI 305
QY 139 DSDHCFPLPAMEGATIL 156
Db 306 RSIRCLPL---EGQAVL 320

RESULT 43
Q26489 PRELIMINARY; PRT; 1299 AA.
ID Q26489
AC Q26489;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; Z68888; CAA93116.1; -
DR PIR; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR011031; Multihem cyt.
DR InterPro; IPR000209; Pept S8 S53.
DR InterPro; IPR009020; Prot_inh_propept.
DR InterPro; IPR002884; Pprotnconverter.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01483; P proproteain; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 3.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1299 AA; 142019 MW; 4C3799C7BEC572AB CRC64;

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
Best Local Similarity 24.1%; Pred. No. 2.3e+02;
Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFDSLHACIPQLRCS-----SNTPLPTCQRYCNAS-----VTNSVKTNAIL-W 57
Db 1150 CSRPLRIDRLNNQVCP---CSRGVNTSPTPTDC-CHCPNGECINSSVAGKRRAEW 1205
QY 58 TGLGLS-----LIISLAV-----EVLMLFLRKISSEPLKDFKNTGSGLLGMAN 101
Db 1206 GALHTAPSADAAPSVAVVTVIAVCAAAVGLFITVLVLIQAHSPEKTRKTSVRG----- 1259
QY 102 IDLEKSTGTDEIILPR-GLGYTVVEECTCDDCIKSKPKVSDH 142

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Db 1260 --VEYSR-----LPRTDVDFTV-----LTSCTDQEGPVEYEH 1289

RESULT 44
Q7R6V0 PRELIMINARY; PRT; 333 AA.
ID Q7R6V0
AC Q7R6V0;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative Yir3 protein.
GN Name=PY07843;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC 1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002953; EAA20383.1; -.
DR InterPro; IPR006477; Yir bir cir.
DR Pfam; PF06022; Cir Bir Yir; 1.
DR TIGRFAMs; TIGR01530; Yir-bir-cir Pla; 1.
SQ SEQUENCE 333 AA; 39110 MW; A3D4B87FF16D7391 CRC64;

Query Match 8.2%; Score 79; DB 2; Length 333;
Best Local Similarity 27.1%; Pred. No. 60;
Matches 57; Conservative 24; Mismatches 79; Indels 50; Gaps 10;

QY 11 NEYFDSLHACIPQLRCSNTPPLPTCQRYCNASVNSVKGYN-----AILWTCGLSL 64
Db 35 NKYCDS--NOCHSDYDRISAGCLYLLDQLYKDSGVIPSPKNSNPYIVDYILWLSYMLNL 92
QY 65 IISLAVFVLMFLRLKISS-----EPLKDFKNTGS-----GLLGMANIDLEKS-RTGD 111
Db 93 INSKEDNITDFYGSHINSCKYKTEISELKNHYHDYGNYYKGL-----IDRRKDFLYND 147
QY 112 EILPR-----GLETVVEEC-----TCEDCIKSKPKVDSHPCHPLPAMERG 152
Db 148 SNIVPKFYEAFLKLCNLNLYNELDNNKNCCKYKLDKNSERPKYKELKDSITNSSPKEML 207
QY 153 AILVTTKNDY---CKSLPAALSATEIK 179
Db 208 STILL--TDYNDPKKCNLSILSYLSAKEK 235

RESULT 45
Q802S1 PRELIMINARY; PRT; 1200 AA.
ID Q802S1
AC Q802S1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE SMC2 protein.
GN Name=smc2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cobbe N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 CC EMBL: AJ534333; CA58848.2; -;
 DR HSSP: P04268; 1IC2.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
 DR GO: GO:0007059; P:chromosome segregation; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR010935; SMC_hinge.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02483; SMC_C; 1.
 DR Pfam: PF06470; SMC_hinge; 1.
 DR Pfam: PF02463; SMC_N; 1.
 DR PRODOM: PD000006; ABC_transporter; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 KW ATP-binding.
 SQ SEQUENCE 1200 AA; 135735 MW; 5243949FD948321EF CRC64;
 Query Match 8.2%; Score 79; DB 2; Length 1200;
 Best Local Similarity 32.3%; Pred. No. 2.3e+02;
 Matches 21; Conservative 8; Mismatches 36; Indels 0; Gaps 0;
 QY 77 LRKISPLKDEPKNTGSGLLGMANIDLEKSRGTDEILPRGLYVTEECTCECIKSKP 136
 DB 578 LNKISATLDRVNTAKSLVGRANVTALSLVGEADLRKMGVFGSTLVCDTLDNAK 637
 QY 137 KVDSD 141
 DB 638 KVAFD 642
 RESULT 46
 ID T13X HUMAN STANDARD; PRT; 293 AA.
 AC O14836;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN Name=TNFRSF13B; Synonyms=TACI;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=93111921;
 RA von Buelow G.-U., Bram R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily.";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION
 RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
 RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
 RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
 RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
 RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
 RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
 RT high affinity receptor for TNF family members APRIL and BlyS.";
 RL J. Biol. Chem. 275:35478-35485(2000).
 RN [4]
 RP FUNCTION
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.S.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [5]
 RP INTERACTIONS WITH TRAF2 AND TRAF5.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.Y., Boyle W.J., Hau H.;
 RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143(2000).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity.
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
 CC intestine and peripheral blood leukocytes. Expressed in resting B-
 CC cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC -----
 CC EMBL: AF023614; AAC51790.1; -;
 DR EMBL: BC028072; AAH28072.1; -;
 DR HSSP: O9Y275; 1OQD.
 DR Genew: HGNC:18153; TNFRSF13B.
 DR MIM: 604907; -;
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001368; TNFR c6
DR PROSITE; PS00452; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;
KW Transmembrane.
FT DOMAIN 1 165 Extracellular (Potential).
FT TRANSMEM 166 186 Signal-anchor for type III membrane protein (Potential).
FT DOMAIN 187 293 Cytoplasmic (Potential).
FT REPEAT 33 67 TNFR-Cys 1.
FT REPEAT 70 104 By similarity.
FT DISULFID 34 47 By similarity.
FT DISULFID 50 62 By similarity.
FT DISULFID 54 66 By similarity.
FT DISULFID 71 86 By similarity.
FT DISULFID 89 100 By similarity.
FT DISULFID 93 104 By similarity.
FT CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).
FT CONFLICT 251 251 P -> L (in Ref. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 8.1%; Score 78.5; DB 1; Length 293;
Best Local Similarity 19.9%; Pred. No. 59;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEVDSLHACIPCOLRCSSTPPLTCQRYCNASVTSVKT--NAILWTCLGLSLI 65
DB 34 CPESQWDLPLGTCWCKTICNHOS-QRTCAAFCSLSCKRQKGFYDHLRLDCISCAI 92

QY 66 I-----SLAVFLMFL-----LRKISSEPLKDFKNTGSLGWANDLEKS---- 107
DB 93 CGQHPKQCAVFCENKLRSPVNLPELRQRSGEVNNSDNGR-YQGLEHKGSEASPALP 151

QY 108 ---RTGDEIILPRG-----LEVTVECTEDCIKSKP-----KVD 139
DB 152 GLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209

QY 140 SDHCFPLPAMEEGATILVTTKTDYIC 165
DB 210 QDH-----AMEAGSVSTSPFVETC 230

RESULT 47
Q8VFW0 PRELIMINARY; PRT; 314 AA.
AC Q8VFW0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor MOR202-16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families."
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073405; AAL61068.1; .
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR Rhodops.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN-1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 34987 MW; DE5CDDF63E3B2FD8 CRC64;

Query Match 8.1%; Score 78.5; DB 2; Length 314;
Best Local Similarity 30.4%; Pred. No. 63;
Matches 31; Conservative 15; Mismatches 41; Indels 15; Gaps 6;

QY 8 CSQNEVDSLHACIPCOLRCSST-----PPLTCQRYCNASVTSVKTNAILWT 58
DB 146 CYMGILQSIHVAFCLSFNCNVINHFCDIPPL-LDISCSDTYTNEL--TVILGT 202

QY 59 CLG-LSLIITSLAVFLMFL--LRKISSEPLKDFKNTGSLGL 97
DB 203 CDGILLVILNTYLLIFAILMRVSEARQAFSTCASHLI 244

RESULT 48
MJK2_METJA STANDARD; PRT; 343 AA.
ID MJK2_METJA
AC Q58752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable potassium channel protein 2 (Mjk2).
GN OrderedLocNames=MJ1357;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
RN [2]
RP FUNCTION.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=22744766; PubMed=12860407;
RA Hellmer J., Zeilinger C.;
RT "MjK1, a K+ channel from M. jannaschii, mediates K+ uptake and K+
RT sensitivity in E. coli."
RL FEBS Lett. 547:165-169(2003).
CC -!- FUNCTION: Probable potassium channel protein.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Contains 1 trkA/RCK domain.
CC -----
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NEW TECHNOLOGICAL DEVELOPMENTS

Search completed: January 28, 2005, 19:57:02
Job time : 220.385 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:52:54 ; Search time 163.743 Seconds
(without alignments)
405.985 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964

Sequence: 1 MLQWAGCQNEYPDSLHA.....CKSLPALSAATEIKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	13	US-10-077-438-1
2	964	100.0	184	13	US-10-077-438-7
3	964	100.0	184	13	US-10-077-137-1
4	964	100.0	184	13	US-10-077-137-7
5	964	100.0	184	14	US-10-068-725-2
6	964	100.0	184	14	US-10-151-882-47
7	964	100.0	184	14	US-10-115-192-8
8	964	100.0	184	14	US-10-008-063-7
9	964	100.0	184	14	US-10-152-363A-27
10	964	100.0	184	14	US-10-216-074-11
11	964	100.0	184	14	US-10-087-080-39
12	964	100.0	184	17	US-10-742-634-9
13	950	98.5	181	9	US-09-854-864-5

14	950	98.5	181	9	US-09-855-158-5	Sequence 5, Appli
15	572	59.3	185	9	US-09-854-864-11	Sequence 11, Appl
16	572	59.3	185	9	US-09-855-158-11	Sequence 11, Appl
17	572	59.3	185	14	US-10-216-074-17	Sequence 17, Appl
18	323	33.5	58	9	US-09-854-864-21	Sequence 21, Appl
19	323	33.5	58	9	US-09-855-158-21	Sequence 21, Appl
20	311.5	32.3	117	9	US-09-854-864-12	Sequence 12, Appl
21	311.5	32.3	117	9	US-09-855-158-12	Sequence 12, Appl
22	286.5	29.7	302	14	US-10-115-192-12	Sequence 12, Appl
23	286	29.7	302	14	US-09-854-864-9	Sequence 9, Appli
24	286	29.7	283	9	US-09-855-158-9	Sequence 9, Appli
25	284	29.5	51	9	US-09-854-864-6	Sequence 6, Appli
26	284	29.5	51	9	US-09-855-158-6	Sequence 6, Appli
27	264	27.4	207	13	US-10-077-438-3	Sequence 3, Appli
28	264	27.4	207	13	US-10-077-137-3	Sequence 3, Appli
29	201	20.9	34	9	US-09-854-864-7	Sequence 7, Appli
30	201	20.9	34	9	US-09-855-158-7	Sequence 7, Appli
31	201	20.9	81	9	US-09-854-864-13	Sequence 13, Appl
32	201	20.9	81	9	US-09-855-158-13	Sequence 13, Appl
33	187	19.4	281	9	US-09-854-864-10	Sequence 10, Appl
34	187	19.4	281	9	US-09-855-158-10	Sequence 10, Appl
35	158	16.4	42	14	US-10-145-206-197	Sequence 197, App
36	116.5	12.1	175	14	US-10-008-063-13	Sequence 13, Appl
37	116.5	12.1	175	15	US-10-380-703-9	Sequence 9, Appli
38	116.5	12.1	175	16	US-10-469-420-1	Sequence 1, Appli
39	104	10.8	21	9	US-09-854-864-8	Sequence 8, Appli
40	104	10.8	21	9	US-09-855-158-8	Sequence 8, Appli
41	100	10.4	185	14	US-10-251-947-2	Sequence 2, Appli
42	94.5	9.8	185	15	US-10-380-703-5	Sequence 5, Appli
43	93	9.6	184	13	US-10-087-192-984	Sequence 984, App
44	93	9.6	184	14	US-10-008-063-2	Sequence 2, Appli
45	93	9.6	184	14	US-10-152-363A-60	Sequence 60, Appl
46	93	9.6	184	15	US-10-380-703-10	Sequence 10, Appl
47	93	9.6	184	17	US-10-742-634-5	Sequence 5, Appli
48	93	9.6	266	15	US-10-380-703-7	Sequence 7, Appli
49	91	9.4	171	14	US-10-251-947-4	Sequence 4, Appli
50	91	9.4	171	14	US-10-251-947-7	Sequence 7, Appli
51	90.5	9.4	170	14	US-10-251-947-6	Sequence 6, Appli
52	86.5	9.0	332	14	US-10-152-363A-50	Sequence 50, Appl
53	86.5	9.0	858	14	US-10-099-322-135	Sequence 135, App
54	86.5	9.0	858	15	US-10-044-564-135	Sequence 135, App
55	86.5	9.0	867	10	US-09-970-944-37	Sequence 37, Appl
56	86.5	9.0	867	14	US-10-099-322-134	Sequence 134, App
57	86.5	9.0	867	15	US-10-044-564-134	Sequence 134, App
58	84	8.7	332	14	US-10-152-363A-62	Sequence 62, Appl
59	83.5	8.7	404	15	US-10-258-368-15	Sequence 15, Appl
60	83	8.6	348	14	US-10-152-363A-54	Sequence 54, Appl
61	81.5	8.5	186	14	US-10-251-947-14	Sequence 14, Appl
62	80.5	8.4	441	15	US-10-365-620-39	Sequence 39, Appl
63	79.5	8.2	293	9	US-09-779-050A-42	Sequence 42, Appl
64	79.5	8.2	1009	8	US-08-987-689A-2	Sequence 2, Appli
65	79.5	8.2	1009	14	US-10-292-524-2	Sequence 2, Appli
66	79.5	8.2	1009	14	US-10-325-430-9	Sequence 9, Appli
67	79.5	8.2	1009	15	US-10-464-805-1	Sequence 1, Appli
68	79.5	8.2	1009	16	US-10-620-052A-8	Sequence 8, Appli
69	79.5	8.2	1009	17	US-10-473-127-1562	Sequence 1562, Ap
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71	79.5	8.2	1009	17	US-10-473-127-1564	Sequence 1564, Ap
72	79.5	8.2	1009	17	US-10-473-127-1565	Sequence 1565, Ap
73	79.5	8.2	1009	17	US-10-473-127-1566	Sequence 1566, Ap
74	79.5	8.2	1009	17	US-10-473-127-1567	Sequence 1567, Ap
75	79.5	8.2	1009	17	US-10-473-127-1568	Sequence 1568, Ap
76	79.5	8.2	1009	17	US-10-473-127-1569	Sequence 1569, Ap
77	78.5	8.1	293	9	US-09-879-919-22	Sequence 22, Appl
78	78.5	8.1	293	9	US-09-854-864-14	Sequence 14, Appl
79	78.5	8.1	293	9	US-09-855-158-14	Sequence 14, Appl
80	78.5	8.1	293	10	US-09-961-376-2	Sequence 2, Appli
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82	78.5	8.1	293	13	US-09-855-564-2	Sequence 2, Appli
83	78.5	8.1	293	13	US-10-087-192-1650	Sequence 1650, Ap
84	78.5	8.1	293	13	US-10-084-971-2	Sequence 2, Appli
85	78.5	8.1	293	14	US-10-068-723-4	Sequence 4, Appli
86	78.5	8.1	293	14	US-10-151-882-46	Sequence 46, Appl

87 78.5 8.1 293 14 US-10-293-816-2 Sequence 2, Appli
 88 78.5 8.1 293 14 US-10-008-063-8 Sequence 8, Appli
 89 78.5 8.1 293 14 US-10-152-363A-2 Sequence 2, Appli
 90 78.5 8.1 293 14 US-10-268-951-22 Sequence 22, Appli
 91 78.5 8.1 293 15 US-10-258-368-1 Sequence 1, Appli
 92 78.5 8.1 293 15 US-10-618-797-4 Sequence 4, Appli
 93 78.5 8.1 293 17 US-10-742-634-7 Sequence 7, Appli
 94 78.5 8.1 293 17 US-10-748-112-27 Sequence 27, Appli
 95 78.5 8.1 301 15 US-10-258-368-12 Sequence 12, Appli
 96 78.5 8.1 339 15 US-10-264-237-2773 Sequence 2773, Ap
 97 78.5 8.1 606 16 US-10-437-963-166150 Sequence 166150,
 98 78.5 8.1 1084 9 US-10-437-963-141214 Sequence 141214,
 99 78 8.1 2991 9 US-09-779-050A-43 Sequence 43, Appli
 100 77.5 8.0 334 15 US-10-258-368-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-077-438-1

; Sequence 1, Application US/10077438

; Publication No. US20020165156A1

; GENERAL INFORMATION:

; APPLICANT: Mackay, Fabienne

; APPLICANT: Browning, Jeffrey

; APPLICANT: Ambrose, Christine

; APPLICANT: Tschoep, Jurg

; APPLICANT: Schneider, Pascal

; APPLICANT: Thompson, Jeffrey

; APPLICANT: Biogen, Inc.

; APPLICANT: Apotech R&D S.A.

; TITLE OF INVENTION: Baff Receptor (BCMA), An

; FILE REFERENCE: A080PCT

; CURRENT APPLICATION NUMBER: US/10/077,438

; CURRENT FILING DATE: 2002-02-18

; PRIOR APPLICATION NUMBER: 60/149,378

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/181,684

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 60/183,536

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 184

; TYPE: PRT

; ORGANISM: homo sapien

US-10-077-438-1

Query Match 100.0%; Score 964; DB 13; Length 184;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLLHACIPQRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Db 1 MLQWAGQCSQNEYFDSLLHACIPQRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFLVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Db 61 GLSLIISLAVFLVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Db 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184

Db 181 ISAR 184

RESULT 2

RESULT 3

US-10-077-137-1

; Sequence 1, Application US/10077137

; Publication No. US20020172674A1

; GENERAL INFORMATION:

; APPLICANT: Mackay, Fabienne

; APPLICANT: Browning, Jeffrey

; APPLICANT: Ambrose, Christine

; APPLICANT: Tschoep, Jurg

; APPLICANT: Schneider, Pascal

; APPLICANT: Thompson, Jeffrey

; APPLICANT: Biogen, Inc.

; APPLICANT: Apotech R&D S.A.

; TITLE OF INVENTION: Baff Receptor (BCMA), An

; FILE REFERENCE: A080PCT

; CURRENT APPLICATION NUMBER: US/10/077,137

; CURRENT FILING DATE: 2001-02-15

; PRIOR APPLICATION NUMBER: 60/149,378

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/181,684

US-10-077-438-7
 ; Sequence 7, Application US/10077438
 ; Publication No. US20020165156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mackay, Fabienne
 ; APPLICANT: Browning, Jeffrey
 ; APPLICANT: Ambrose, Christine
 ; APPLICANT: Tschoep, Jurg
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Thompson, Jeffrey
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Apotech R&D S.A.
 ; TITLE OF INVENTION: Baff Receptor (BCMA), An
 ; FILE REFERENCE: A080PCT
 ; CURRENT APPLICATION NUMBER: US/10/077,438
 ; CURRENT FILING DATE: 2002-02-18
 ; PRIOR APPLICATION NUMBER: 60/149,378
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/181,684
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/183,536
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 US-10-077-438-7

Query Match 100.0%; Score 964; DB 13; Length 184;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLLHACIPQRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLLHACIPQRCSSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60
 Qy 61 GLSLIISLAVFLVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFLVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 Qy 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184


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; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-2

Query Match      100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: homo sapiens
US-10-068-725-2

; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindevogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match      100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match      100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47
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US-10-151-882-47

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 7

US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens

US-10-115-192-8

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 8

US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1

GENERAL INFORMATION:

; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Heme, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-008-063-7

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 9

US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-152-363A-27

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Db	121	YTVEECTCEDC1KSPKPKVDSHCFFLPAMEEGATILVTTTKNDYCKSLPAALSATEIEKS
Qy	181	ISAR 184
Db	181	ISAR 184

RESULT 10

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US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

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Query Match	100.0%	Score 964;	DB 14;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 2.7e-90;		
Matches 184;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLWAGQCSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNASVTVSKGTNAILWTCL	60	
Db	1	MLWAGQCSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNASVTVSKGTNAILWTCL	60	
Qy	61	GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKRTGDEIILPRGLE	120	
Db	61	GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKRTGDEIILPRGLE	120	
Qy	121	YTVVEECTCEDCICKSPKVDSDHCPFLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180	
Db	121	YTVVEECTCEDCICKSPKVDSDHCPFLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180	
Qy	181	ISAR	184	
Db	181	ISAR	184	

RESIT.T 11

RES0111
US-10-087-080-39 .
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555

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; PROR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor nec
; -OTHER INFORMATION: 17 (TNFRS
US-10-087-080-39

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Query Match	100.0%;	Score 964;	DB 14;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 2.7e-90;		
Matches 184; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MLQWAGCQNEYPFDSLHLHACIPQLRCSNTPPLTCORYCNASVTNSVKGTTNAIILWTCL	60	
Db	1	MLQWAGCQNEYPFDSLHLHACIPQLRCSNTPPLTCORYCNASVTNSVKGTTNAIILWTCL	60	
Qy	61	GLSLIIISLAVFVLMPFLIRKISSBPLKDEPKNTGSGLLIGMANIDLEKSRTGDEILPRGLE	120	
Db	61	GLSLIIISLAVFVLMPFLIRKISSBPLKDEPKNTGSGLLIGMANIDLEKSRTGDEILPRGLE	120	
Qy	121	YTVBEECTCEDCIKSPKVDSHDHFPLPAMEEGATILVTTKTNDYCKSLPAALSATELEKS	180	
Db	121	YTVBEECTCEDCIKSPKVDSHDHFPLPAMEEGATILVTTKTNDYCKSLPAALSATELEKS	180	
Qy	181	ISAR	184	
Db	181	ISAR	184	

RESULT 12

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US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-1alpha
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742-634-9
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/433,341
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/466,841
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

```

	Query Match	100.0%;	Score 964;	DB 17;	Length 184;		
	Best Local Similarity	100.0%;	Pred. No. 2.7e-90;				
	Matches 184;	Conservative	0;	Mismatches	0; Indels	0; Gaps	0;
Qy	1	MLQWAGCQNEFYDSLHACIPQLRCSNSTPPLTCQRYCNASVTNSVKGTTNAILWTCL	60				
Db	1	MLQWAGCQNEFYDSLHACIPQLRCSNSTPPLTCQRYCNASVTNSVKGTTNAILWTCL	60				
Qy	61	GLSLIISLAVFLWMFLLRKISSPELKDFPKNTGSGLLGMANIDLEKSRTGDEILPRGLE	120				
Db	61	GLSLIISLAVFLWMFLLRKISSPELKDFPKNTGSGLLGMANIDLEKSRTGDEILPRGLE	120				
Qy	121	YTVBECTCEDCIKSPKVDSHDHFPIPAAMEEGATILVTTKNDYCYSLPALSALETEIKS	180				

Db 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 13
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 98.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 7.1e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCIGLS 63
Db 1 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCIGLS 60
QY 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 123
Db 61 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 120
QY 124 ECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
Db 121 ECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
QY 184 R 184
Db 181 R 181

RESULT 15
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCIGLS 63
Db 1 MAQCQFHESEYFDSLHACPKHLRCSN--PPATCQPCYCDPSVTSSVKGTVTVLWIFLGT 58
QY 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGL 119
Db 59 LVLSLALFTISFLRLKRNFEALKDEPQPCQLDGSQQLKADTELTRIRAGDDRIIPRSL 118
QY 120 EYTVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSVPTALQSVGM 178
QY 178 EKSISAR 184
Db 179 EKPHTHR 185

RESULT 16
US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1

Db 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 14
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT

```
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match      59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAQCQFSEYFDSLHACKPCHLRCN--PPATCQPYCDPSVTSSVKGTTVTLWIFLGLT 58

Qy 64 LIISLAVFLMFLRKISSEPLKDEPKN----TCGSLGGMANIDLEKSRGTGDEILPRGL 119
Db 59 LVLSLALFTISFLLRKNPEALKDEPQSGLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVECTCEDCVKSPKGDSDHFFPLPAMEEGATILVTTKTGDKSSVPTALQSVNMG 178

Qy 178 EKSISAR 184
Db 179 EKPTHTR 185

Query Match      59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAQCQFSEYFDSLHACKPCHLRCN--PPATCQPYCDPSVTSSVKGTTVTLWIFLGLT 58

Qy 64 LIISLAVFLMFLRKISSEPLKDEPKN----TCGSLGGMANIDLEKSRGTGDEILPRGL 119
Db 59 LVLSLALFTISFLLRKNPEALKDEPQSGLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVECTCEDCVKSPKGDSDHFFPLPAMEEGATILVTTKTGDKSSVPTALQSVNMG 178

Qy 178 EKSISAR 184
Db 179 EKPTHTR 185

Query Match      59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAQCQFSEYFDSLHACKPCHLRCN--PPATCQPYCDPSVTSSVKGTTVTLWIFLGLT 58

Qy 64 LIISLAVFLMFLRKISSEPLKDEPKN----TCGSLGGMANIDLEKSRGTGDEILPRGL 119
Db 59 LVLSLALFTISFLLRKNPEALKDEPQSGLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVECTCEDCVKSPKGDSDHFFPLPAMEEGATILVTTKTGDKSSVPTALQSVNMG 178

Qy 178 EKSISAR 184
Db 179 EKPTHTR 185

Query Match      59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLS 63
Db 1 MAQCQFSEYFDSLHACKPCHLRCN--PPATCQPYCDPSVTSSVKGTTVTLWIFLGLT 58
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Qy 64 LIISLAVFLMFLRKISSEPLKDEPKN----TCGSLGGMANIDLEKSRGTGDEILPRGL 119
Db 59 LVLSLALFTISFLLRKNPEALKDEPQSGLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVECTCEDCVKSPKGDSDHFFPLPAMEEGATILVTTKTGDKSSVPTALQSVNMG 178

Qy 178 EKSISAR 184
Db 179 EKPTHTR 185
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RESULT 18

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US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21
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Query Match      33.5%; Score 323; DB 9; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLSLI 65
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTTNAILWTCLGLSLI 58
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RESULT 19

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US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21
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Query Match      33.5%; Score 323; DB 9; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
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RESULT 22

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/ PRIOR FILLING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/157933
/ PRIOR FILLING DATE: 1999-10-06
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-115-192-12

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[illegible]

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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864

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; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 29.7%; Score 286; DB 9; Length 283;
Best Local Similarity 37.6%; Pred. No. 1e-20;
Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTAIWTCLGLS 63
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA----- 51

Qy 64 LIISLAVFLMFLLRKISSEPLKDEFKNTGSG-----LLGMANIDLEKSRGTG 110
Db 52 -----GGGGDKTHTCPPCAPPELLGGPSVFLFPKPK 84

Qy 111 DEILPRGLEVTVECTCEDCIKPKVDSD-----HCFPLPAMEE-----GATIL 156
Db 85 DTLMISRTPEVT---CVVVDVSHEDPVEKFNWYVDGVEVHNNAKTKPREEQNSTYRVSV 141

Qy 157 VTTKTNDY-----CKSLPAALSATEIEKSI 182
Db 142 LTVLHQDLNGKEYCKVKNKALPA-PIEKTIS 173

RESULT 24

US-09-855-158-9
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match 29.7%; Score 286; DB 9; Length 283;
Best Local Similarity 37.6%; Pred. No. 1e-20;
Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTAIWTCLGLS 63
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA----- 51

Qy 64 LIISLAVFLMFLLRKISSEPLKDEFKNTGSG-----LLGMANIDLEKSRGTG 110
Db 52 -----GGGGDKTHTCPPCAPPELLGGPSVFLFPKPK 84

Qy 111 DEILPRGLEVTVECTCEDCIKPKVDSD-----HCFPLPAMEE-----GATIL 156
Db 85 DTLMISRTPEVT---CVVVDVSHEDPVEKFNWYVDGVEVHNNAKTKPREEQNSTYRVSV 141

Qy 157 VTTKTNDY-----CKSLPAALSATEIEKSI 182
Db 142 LTVLHQDLNGKEYCKVKNKALPA-PIEKTIS 173

RESULT 25

US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 29.5%; Score 284; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA 54
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA 51

RESULT 26

US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match 29.5%; Score 284; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA 54
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGTA 51

RESULT 27

US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match 27.4%; Score 264; DB 13; Length 207;
Best Local Similarity 63.9%; Pred. No. 1.2e-18;
Matches 53; Conservative 2; Mismatches 0; Indels 28; Gaps 2;

QY 1 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTPLTCQRYC 40
DB 39 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPTPLTCCLHACIPQCLRCSSNTPTPLTCQRY 98

QY 41 CNASVTNSVKG-----TNAI 55
DB 99 CNASVTNSVKGQRYCNASVTNSV 121

RESULT 28
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT

; ORGANISM: homo sapien
US-10-077-137-3

Query Match 27.4%; Score 264; DB 13; Length 207;
Best Local Similarity 63.9%; Pred. No. 1.2e-18;
Matches 53; Conservative 2; Mismatches 0; Indels 28; Gaps 2;

QY 1 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTPLTCQRY 40
DB 39 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPTPLTCCLHACIPQCLRCSSNTPTPLTCQRY 98

QY 41 CNASVTNSVKG-----TNAI 55
DB 99 CNASVTNSVKGQRYCNASVTNSV 121

RESULT 29
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 20.9%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 34

RESULT 30
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7


```
Query Match      20.9%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
   |||||
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 31
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      20.9%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
   |||||
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 32
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match      20.9%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
   |||||
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
```

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RESULT 33
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      19.4%; Score 187; DB 9; Length 281;
Best Local Similarity 29.8%; Pred. No. 1.4e-10;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

Qy 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNA5VTNSVKGTHAILWTCLGLS 63
   |||||
Db 1 MAGQCFHSEYFDSLHACKFCHLRCSN--PPTCQPYCDPSVTSSVKGK----- 47

Qy 64 LIISLAVFLMFLRLKISSEPLKDEPKNTGSG-----YTGSGGDKTHCTPCPAPPELLGSPSVFLPPK 108
   |||||
Db 48 -----YTGSGGDKTHCTPCPAPPELLGSPSVFLPPK 80

Qy 109 TGDEIILPRGLVTVBECTCEDCIKSPKVDSD-----HCFPLPAMBE-----GAT 154
   |||||
Db 81 PKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYDGVGVHNAKTRPBEQYNSTYRVV 137

Qy 155 ILVTTKTINDY-----CKSLPAALSATETEKSTIS 182
   |||||
Db 138 SVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIIS 171

RESULT 34
US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match      19.4%; Score 187; DB 9; Length 281;
Best Local Similarity 29.8%; Pred. No. 1.4e-10;
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; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-8

Query Match      10.8%; Score 104; DB 9; Length 21;
Best Local Similarity 100.0%; Pred.No. 0.0016;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          55 ILWTCGLGSLIISLAVFVLMF 75
            |||||
Db           1  ILWTCGLGSLIISLAVFVLMF 21


RESULT 41
US-10-251-947-2
; Sequence 2, Application US/10251947
; Publication No. US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-2

Query Match      10.4%; Score 100; DB 14; Length 185;
Best Local Similarity 23.8%; Pred.No. 0.065;
Matches 44; Conservative 25; Mismatches 62; Indels 54; Gaps 8;

QY          8 CSONEYFDLLHACIPQCRLCSNTPPLTCCORYCNASVTNSVKGT-----52
             :|:|:|:|:~::~::
Db         19 CVPTECYDLLVRKCVDCRLLRS--PPKTA----AGASSPAPGALTALQPQESVGTCGEV 71
               |:||:||||:|:~::~::
QY        53 ----NAILM---TCIGLSLIISLAVFLMLLRKKISSSEPLKDPEFKNTGGSLICMANIDLE 105
              :|:|:|:|:~::~::
Db       72 SLPLGPLLGCPAILGLVLVALVLVLGV-----SWRRQRQLRGAASTE-- 116
                |||||
QY        106 KSRTGDEIIILPRGLETVV--EECTCEDCIKSXPKVDSD-----HCFFLPAMEEGCATIL 156
              :|:|:|:|:~::~::
Db       117 -APDGDKAAPBPLDKVIILSPGTTDATAPAWPPPGEDQGCTPPPGHSIVPVATELGSTEL 175
                |||||
QY        157 VTKKT 161
              |||||
Db       176 VTGTK 180


RESULT 42
US-10-380-703-5
; Sequence 5, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
```

; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-5

Query Match 9.8%; Score 94.5; DB 15; Length 185;
Best Local Similarity 25.8%; Pred. No. 0.24; Indels 49; Gaps 8;
Matches 47; Conservative 22; Mismatches 64; Indels 49; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTC---QRYCNASVTNSVKGTHAI 55
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 56 LW---TCGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEK 106
DB 79 LFGAPALLGLALVLVLVGLVSWRRORRLRGASSAEPDGDKDAPEPL----- 128
QY 107 SRTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCHCFPLPAMEEGATILVTT 159
DB 129 ----DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTT 177
QY 160 KT 161
DB 178 KT 179

RESULT 43
US-10-087-192-984
; Sequence 984, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 984
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-984

Query Match 9.6%; Score 93; DB 13; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTC---PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 57 W---TCGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
DB 79 FGAPALLGLALVLVLVGLVSWRRORRLRGASSAEPDGDKDAPEPL----- 127
QY 108 RTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCHCFPLPAMEEGATILVTTK 160
DB 128 ---DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTTK 177
QY 161 T 161
DB 178 T 178

RESULT 44
US-10-008-063-2
; Sequence 2, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Heme, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-2

Query Match 9.6%; Score 93; DB 14; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTC---PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 57 W---TCGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
DB 79 FGAPALLGLALVLVLVGLVSWRRORRLRGASSAEPDGDKDAPEPL----- 127
QY 108 RTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCHCFPLPAMEEGATILVTTK 160
DB 128 ---DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTTK 177
QY 161 T 161
DB 178 T 178

RESULT 45
US-10-152-363A-60
; Sequence 60, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-60

Query Match 9.6%; Score 93; DB 14; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTC---PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78

Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVLGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTP-----GHSVPVPATELGSGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 46
US-10-380-703-10
; Sequence 10, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-10

Query Match 9.6%; Score 93; DB 15; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSNTP--PLTCORYCNASVTNSVKGTTAIL 56
Db 19 CVPACFDLLVRHCVACGLLRTPRPKPAGASSAPRPTALQPQSVGAGAGEAALPLPGLL 78
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVLGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTP-----GHSVPVPATELGSGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 47
US-10-742-634-5
; Sequence 5, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Th

FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-5

Query Match 9.6%; Score 93; DB 17; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSNTP--PLTCORYCNASVTNSVKGTTAIL 56
Db 19 CVPACFDLLVRHCVACGLLRTPRPKPAGASSAPRPTALQPQSVGAGAGEAALPLPGLL 78
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVLGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTP-----GHSVPVPATELGSGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 48
US-10-380-703-7
; Sequence 7, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-7

Query Match 9.6%; Score 93; DB 15; Length 266;
Best Local Similarity 26.5%; Pred. No. 0.53;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSNTP--PLTCORYCNASVTNSVKGTTAIL 56
Db 101 CVPACFDLLVRHCVACGLLRTPRPKPAGASSAPRPTALQPQSVGAGAGEAALPLPGLL 160
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:45:08 ; Search time 7.48624 Seconds
(without alignments)
436.984 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201

Sequence: 1 CSQNEYDLSLHACIPQLRCSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR_79:*

2: PIR1:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	184	2 S43486	B-cell maturation
2	67.5	33.6	1548	2 S34583	serine proteinase
3	64.5	32.1	5376	2 T42215	zonadhesin - mouse
4	61	30.3	1101	2 T16840	hypothetical prote
5	59	29.4	1758	2 T15577	hypothetical prote
6	58	28.9	1299	2 T43251	furin (EC 3.4.21.7
7	57.5	28.6	63	2 S07127	chymotrypsin/elast
8	57.5	28.6	1680	2 A43434	furin (EC 3.4.21.7
9	57	28.4	1717	1 A45558	epidermal growth f
10	56	27.9	2476	2 T34022	zonadhesin - pig
11	55.5	27.6	989	2 T01519	hypothetical prote
12	55	27.4	330	2 T25169	hypothetical prote
13	55	27.1	1513	2 T23691	hypothetical prote
14	54.5	27.1	2155	2 T30197	alpha tectorin - m
15	54	26.9	1980	2 S54307	myosin-heavy chain
16	54	26.9	2022	2 A59256	myosin-IXb [simila
17	53.5	26.6	758	2 S46625	finger protein IJL
18	53	26.4	1574	2 T13954	MEGF6 protein - ra
19	53	26.4	2824	2 T22759	hypothetical prote
20	52.5	26.1	118	2 S61051	hypothetical prote
21	52	25.9	255	2 A84544	hypothetical prote
22	52	25.9	294	2 T23682	hypothetical prote
23	52	25.9	547	2 T34318	hypothetical prote
24	52	25.9	1474	2 D88550	protein ZC84.6 [im
25	52	25.9	2844	2 S28291	hypothetical prote
26	51.5	25.6	63	2 S57816	antimicrobial pept
27	51.5	25.6	282	2 T48763	slah-1A protein -
28	51.5	25.6	282	2 S35754	slah-1B protein -
29	51.5	25.6	497	2 T27827	hypothetical prote

30	51.5	25.6	915	2	T21773	hypothetical prote
31	51.5	25.6	927	2	T21772	hypothetical prote
32	51.5	25.6	999	2	T19275	hypothetical prote
33	51.5	25.6	2120	2	T30243	alpha tectorin - c
34	51	25.4	641	2	E96612	probable transcrip
35	51	25.4	653	2	G96675	hypothetical prote
36	51	25.4	746	2	G84605	hypothetical prote
37	50.5	25.1	610	1	I46001	C4b-binding protei
38	50	24.9	63	2	S08572	chymotrypsin/elast
39	50	24.9	74	2	S10332	ubiquitin / riboso
40	50	24.9	342	2	T30370	hypothetical prote
41	50	24.9	376	2	C81272	probable aminotran
42	50	24.9	455	1	GQHTU1	tumor necrosis fac
43	50	24.9	561	2	T27318	hypothetical prote
44	50	24.9	626	2	T27319	hypothetical prote
45	50	24.9	922	2	T23573	hypothetical prote
46	50	24.9	1360	2	F96596	hypothetical prote
47	49.5	24.6	216	2	G83398	probable two-compo
48	49.5	24.6	392	2	T27303	hypothetical prote
49	49.5	24.6	1847	2	T30558	resistance protein
50	49	24.4	189	2	T48828	hypothetical prote
51	49	24.4	283	2	T22272	hypothetical prote
52	49	24.4	306	2	B71439	hypothetical prote
53	49	24.4	321	1	S28390	homeotic protein m
54	49	24.4	346	2	T20458	hypothetical prote
55	49	24.4	350	2	JC5828	paired-box-contain
56	49	24.4	447	2	A96639	protein TIF3.18 [i
57	49	24.4	461	2	J44302	tumor necrosis fac
58	49	24.4	602	2	T47794	hypothetical prote
59	49	24.4	654	2	T30136	hypothetical prote
60	49	24.4	1483	2	S30015	hypothetical prote
61	49	24.4	1620	2	T27283	hypothetical prote
62	49	24.4	1984	2	T13171	probable vitelloge
63	49	24.4	2531	2	A46019	notch-1 protein -
64	49	24.4	3635	2	T10053	laminin alpha 5 ch
65	48.5	24.1	474	2	T27297	hypothetical prote
66	48.5	24.1	608	1	ABONS1	serum albumin 1 pr
67	48.5	24.1	608	1	ABONS2	serum albumin 2 pr
68	48.5	24.1	1846	2	T33079	hypothetical prote
69	48.5	24.1	3034	2	T14119	seven-pass transme
70	48	23.9	56	2	JN0380	trypsin inhibitor
71	48	23.9	98	2	C89046	protein C10G8.4 [i
72	48	23.9	304	1	JC2264	tissue factor path
73	48	23.9	314	2	T27686	hypothetical prote
74	48	23.9	450	1	TVFVNR	protein kinase (EC
75	48	23.9	513	2	D88991	protein apx-1 [imp
76	48	23.9	539	2	T01513	Crp synthase (EC 6
77	48	23.9	596	2	F88188	protein C18H9.7 [i
78	48	23.9	597	2	T08681	adenosylhomocystei
79	48	23.9	661	2	E71427	hypothetical prote
80	48	23.9	666	2	T30098	hypothetical prote
81	48	23.9	681	2	B53542	brefeldin A-sensit
82	48	23.9	689	2	T52060	protein MEDEA [imp
83	48	23.9	962	2	JC5571	subtilisin-like pr
84	48	23.9	969	1	A39490	subtilisin-like pr
85	48	23.9	975	2	JC5570	subtilisin-like pr
86	48	23.9	1034	2	JC5598	mucin - rat
87	48	23.9	1079	1	TVFVMI	gag-Rml1-env polyp
88	48	23.9	1203	2	A49175	Notch B protein -
89	48	23.9	1797	2	A55677	laminin beta-2 cha
90	47.5	23.6	249	2	T25843	hypothetical prote
91	47.5	23.6	275	2	T51437	hypothetical prote
92	47.5	23.6	355	1	S22181	gamma-1-microglobu
93	47.5	23.6	546	2	S67292	probable membrane
94	47.5	23.6	837	2	S43656	furin (EC 3.4.21.7
95	47.5	23.6	1188	2	D86236	protein P14N23.5 [
96	47.5	23.6	1798	2	S53869	laminin beta-2 cha
97	47.5	23.6	2180	2	T29764	hypothetical prote
98	47.5	23.6	2823	2	F87908	protein T22A3.8 [i
99	47.5	23.6	2823	2	T23064	hypothetical prote
100	47.5	23.6	3102	2	T43291	laminin alpha chai

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N/Alternate names: BCM protein, BCMA protein; BEL protein
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C/Accession: S43486; S31208; S36661
R/Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A/Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectional
A/Reference number: S43486; MUID:94218235; PMID:8165126
A/Accession: S43486
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-184 <LAA>
A/Cross-references: UNIPROT:Q02223; EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471244
R/Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
EMBO J. 11, 3897-3904, 1992
A/Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(p21;p11)
A/Reference number: S31208; MUID:93010984; PMID:1396583
A/Accession: S31208
A/Molecule type: mRNA
A/Residues: 1-184 <LA2>
A/Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A/Accession: S36661
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 4-184 <LA3>
A/Cross-references: EMBL:Z14955
C/Genetics:
A/Genes: GDB:BCMA
A/Cross-references: GDB:135977; OMIM:109545
A/Map position: 16p13.1-16p13.1
A/Introns: 44/1, 93/1
C/Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.2e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 2
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S34583
R/Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A/Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a serine proteinase
A/Reference number: S34583; MUID:93327934; PMID:8335106
A/Accession: S34583
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1548 <NAK>
A/Cross-references: UNIPROT:Q04592; GB:D17583; NID:G407344; PIDN:BA04507.1; PID:d100503
C/Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.4; Indels 14; Gaps 1;
Matches 14; Conservative 4; Mismatches 4

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 32
DB 1152 CAAVEWDEGSHRCQPCCHKKCRCSGSPSEDQCYTCPR 1188

RESULT 3
T42215
zonadhesin - mouse
N/Alternate names: sperm-specific membrane protein
C/Species: Mus musculus (house mouse)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42215
R/Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A/Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
A/Reference number: Z22080; MUID:98123114; PMID:9452463
A/Accession: T42215
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-5376 <GAO>
A/Cross-references: UNIPROT:O88799; EMBL:U97068; NID:G3327420; PID:G3327421; PIDN:AAAC2661
C/Genetics:
A/Genes: Zan
A/Map position: 5
C/Function:
A/Description: functions in multiple cell adhesion processes
A/Note: found exclusively on the apical region of the sperm head
C/Keywords: cell adhesion

Query Match 32.1%; Score 64.5; DB 2; Length 5376;
Best Local Similarity 35.1%; Pred. No. 16; Indels 3; Gaps 2;
Matches 13; Conservative 5; Mismatches 16

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 3300 CPTNSQFTDCLPSCVPSNRCVTSVPSVSSCREGC 3336

RESULT 4
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16840
R/Geisel, C.
submitted to the EMBL Data Library, October 1995
A/Description: The sequence of C. elegans cosmid T10E10.
A/Reference number: Z18588
A/Accession: T16840
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1101 <GEI>
A/Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:G1049339; PID:G1049343; PIDN:AAA803
C/Genetics:
A/Genes: CESP:T10E10.4
A/Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 30.3%; Score 61; DB 2; Length 1101;
Best Local Similarity 37.5%; Pred. No. 11; Indels 2; Gaps 1;
Matches 12; Conservative 7; Mismatches 11

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 30
DB 351 CSQSTVFNSDLNVCVPLAIONSCDSSTQCPVC 382

RESULT 5
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15577
R/Latreille, P.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C23G10.
A/Reference number: Z18372

[illegible]

A;Map position: 5
A;Introns: 16/3
C;Superfamily: gliadin

Query Match 27.4%; Score 55; DB 2; Length 330;
Best Local Similarity 28.6%; Pred. No. 21;
Matches 12; Conservative 7; Mismatches 15; Indels 8; Gaps 2;

QY 1 CSQNEYFDSLHACIP-----COLRCSSNTPL---TCORYC 34
| : : : | : : : || : |
Db 59 CASSQQVQLQTSQMCPAQCSQCQSQSNTTCCQTCCQSC 100

RESULT 13
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:O17970; EMBL:Z81573; PIDN:CA804625.1; GSPDB:GN000020
A;Experimental source: clone M02G9
C;Genetics:
A;Gene: CRSP.M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 27.4%; Score 55; DB 2; Length 1513;
Best Local Similarity 44.8%; Pred. No. 76;
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

QY 8 DSSLHAC-IPCQLRC-SSNTPLPTCORYC 34
|| : | || | || | || : |
Db 141 DSQNVCNVCGAGCVSQNSPPAVCQOTC 169

RESULT 14
T30197
alpha tectorin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30197
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous
A;Reference number: Z20771; MUID:97236843; PMID:9079715
A;Accession: T30197
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: mRNA
A;Residues: 1-2155 <LEG>
A;Cross-references: UNIPROT:Q08523; EMBL:X99805; NID:g1915908; PIDN:CAA68138.1;
A;Experimental source: strain CD1; whole cochlea
A;Note: non-collagenous protein only expressed in the inner ear, by cells both

Query Match 27.1%; Score 54.5; DB 2; Length 2155;
Best Local Similarity 29.4%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLPTCORYC 34
| | : : : | | : : : || : |
Db 1372 CPPNSHYECSVCQP---RCAAIRLKSDCNHYC 1402

RESULT 15
S54307
myosin heavy chain - rat
C;Species: Rattus norvegicus (Norway rat)

C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S54307
R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A>Title: A novel type of myosin implicated in signalling by rho family GTPases.
A/Reference number: S54307; MUID:95188874; PMID:7882973
A/Accession: S54307
A>Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1980 <REI>
A/Cross-references: UNIPROT:Q63358; EMBL:X77609; NID:G639998; PIDN:CAA54700.1; PID:G639998
C/Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z
C/Keywords: nucleotide binding; P-loop
F:149-942/Domain: myosin motor domain homology <MMOT>
F:239-246/Region: nucleotide-binding motif A (P-loop)
F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 26.9%; Score 54; DB 2; Length 1980;
Best Local Similarity 52.9%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCOLRCSSNTPPLTCOR 32
DB 1812 PCLLRCPDSDPLTSMK 1828
||| ||| |. ||| :
||| ||| |. ||| :

RESULT 16
A59256
myosin-Ixb [similarity] - human
C/Species: Homo sapiens (man)
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: A59256; I61700
R:Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.
J. Cell Sci. 109, 653-661, 1996
A>Title: Human myosin-Ixb, an unconventional myosin with a chimerin-like rho/rac GTPase-
A/Reference number: A59256; MUID:97063843; PMID:8907710
A/Accession: A59256
A>Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-2022 <WIR>
A/Cross-references: UNIPROT:Q14788; GB:U42391; NID:G1147782; PIDN:AAC50402.1; PID:gl1477
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A>Title: Identification and overlapping expression of multiple unconventional myosin gen
A/Reference number: A55758; MUID:94294418; PMID:8022818
A/Accession: I61700
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 234-322 <RES>
A/Cross-references: GB:I29149; NID:G457257; PIDN:AAA20912.1; PID:G531142
C/Genetics:
A/Gene: GDB:MYO9B; OMIM:602129
A/Map position: 19p13.1
C/Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z
C/Keywords: nucleotide binding; P-loop
F:149-941/Domain: myosin motor domain homology #status atypical <MMO>
F:239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 26.9%; Score 54; DB 2; Length 2022;
Best Local Similarity 52.9%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCOLRCSSNTPPLTCOR 32
DB 1852 PCLLRCPDSDPLTSMK 1868
||| ||| |. ||| :
||| ||| |. ||| :

RESULT 17
S46625
finger protein YUL206c - yeast (Saccharomyces cerevisiae)
N/Alternate names: probable membrane protein YUL206c; protein J0316
C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004

A;Molecule type: mRNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q06985; EMBL:Z19580; NID:g297801; PIDN:CAA79633
C;Superfamily: Drosophila developmental protein sine; RING finger homology
Query Match 25.6%; Score 51.5; DB 2; Length 282;
Best Local Similarity 41.9%; Pred. NO. 48;
Matches 13; Conservative 3; Mismatches 12; Indels 3; Gaps
OV 7 F0SLHACIPCO---LRCSNSTPPLTCQRYC 34

RESULT 31
T21772

D**b** 516 YEDSLKTCIGRAFERVKMTPLRIQSY 54

RESULT 33

T30243

alpha tectorin - chicken

C;Species: Gallus gallus (chicken)

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T30243

R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.

Hear. Res. 130, 62-74, 1999

A;Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.

A;Reference number: Z20783; MUID:99251817; PMID:10320099

A;Accession: T30243

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2120 <COU>

A;Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:el361092; PIDN:CAAG

A;Note: non-collagenous protein only expressed in the inner ear

Query Match 25.6%; Score 51.5; DB 2; Length 2120;

Best Local Similarity 31.4%; Pred. No. 2.7e+02;

Matches 11; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEYFDSLHACIP-CQLRCSNTPTLTCQRYC 34

DB 1345 CPNSHYES-----CVSLCQPRCAIRLKSDCGHYC 1375

RESULT 34

E96612

probable transcription factor F12K22.14 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E96612

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96612

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-641 <STO>

A;Cross-references: UNIPROT:Q9FV33; GB:AE005173; NID:gl1079528; PIDN:AAG29238.1; GSPDB:G

C;Genetics:

A;Map position: 1

C;Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger

Query Match 25.4%; Score 51; DB 2; Length 641;

Best Local Similarity 45.8%; Pred. No. 1.1e+02;

Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

QY 15 IPCQ-----LRCSSNTPTP---LTC 30

DB 7 LPCCDGVGVCMRCKSNPPPEESLTC 30

RESULT 35

G96675

hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G96675

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96675

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-653 <STO>

A;Cross-references: UNIPROT:Q9S9J8; GB:AE005173; NID:g4646199; PIDN:AAD26872.1; GSPDB:GN

C;Genetics:

A;Gene: T23K8.9

A;Map position: 1

Query Match 25.4%; Score 51; DB 2; Length 653;

Best Local Similarity 42.3%; Pred. No. 1.1e+02;

Matches 11; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 7 FDSLHACIP-----QLRCSNTPTPL 28

DB 204 FDEMFFVCSACNFLLDLRCSVLPPL 229

RESULT 36

G84605

hypothetical protein At2g21840 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84605

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10611717

A;Accession: G84605

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-746 <STO>

A;Cross-references: UNIPROT:Q9SJ15; GB:AE002093; NID:g4417278; PIDN:AAD20403.1; GSPDB:GN

C;Genetics:

A;Gene: At2g21840

A;Map position: 2

Query Match 25.4%; Score 51; DB 2; Length 746;

Best Local Similarity 28.6%; Pred. No. 1.3e+02;

Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRC 21

DB 267 CKETVVYDRFYLCVCECLKC 287

RESULT 37

I46001

C4b-binding protein alpha chain - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I46001; S43190

R;Hillarp, A.; Thern, A.; Dahlback, B.

J. Immunol. 153, 4190-4199, 1994

A;Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains pro

A;Reference number: I46001; MUID:95015909; PMID:7930621

A;Accession: I46001

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-610 <HIL>

A;Cross-references: UNIPROT:Q28065; EMBL:Z31693; NID:g469117; PIDN:CAA83498.1; PID:g46911

C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology

F;50-107/Domain: complement factor H repeat homology <FHL>

F;112-169/Domain: complement factor H repeat homology <FH2>

F:174-234/Domain: complement factor H repeat homology <PH3>
 F:239-294/Domain: complement factor H repeat homology <PH4>
 F:299-362/Domain: complement factor H repeat homology <PH5>
 F:366-425/Domain: complement factor H repeat homology <PH6>
 F:429-483/Domain: complement factor H repeat homology <PH7>
 F:487-541/Domain: complement factor H repeat homology <PH8>

Query Match 25.1%; Score 50.5; DB 1; Length 610;
 Best Local Similarity 32.4%; Pred. No. 1.2e+02;
 Matches 12; Conservative 5; Mismatches 9; Indels 11; Gaps 1;

QY 6 YFSLHAC-----IPQLRCSNTPPLTCQ 31
 DB 259 YQSSIVYACNGKRLGDSLIHCEADNSWNPPTCE 295

RESULT 38
 S08572
 chymotrypsin/elastase inhibitor - common roundworm
 C:Species: Ascaris lumbricoides (common roundworm)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C:Accession: S08572
 R:Babin, D.R.; Peanasky, R.J.; Goos, S.M.
 Arch. Biochem. Biophys. 232, 143-161, 1984
 A:Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure of the chymotrypsin-like isoform
 A:Reference number: S07127; MUID:84255715; PMID:6564898
 A:Accession: S08572
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-63 <RAB>
 C:Superfamily: roundworm trypsin inhibitor

Query Match 24.9%; Score 50; DB 2; Length 63;
 Best Local Similarity 30.8%; Pred. No. 21;
 Matches 12; Conservative 6; Mismatches 9; Indels 12; Gaps 3;

QY 1 CSQNEYFDSLHACIPQLRCSNTP-----PLTCQ 31
 DB 4 CGKNEVWTE---CTGCELCGQDPTFCALMCRPPSCE 38

RESULT 39
 S10332
 ubiquitin / ribosomal protein CEP52 - common tobacco (fragment)
 N:Alternate names: ubiquitin fusion protein
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C:Accession: S10332
 R:Genschik, P.; Parmentier, Y.; Criqui, M.C.; Fleck, J.
 Nucleic Acids Res. 18, 4007, 1990
 A:Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.
 A:Reference number: S10332; MUID:90326543; PMID:2165257
 A:Accession: S10332
 A:Molecule type: DNA
 A:Residues: 1-74 <GEN>
 A:Cross-references: UNIPROT:P19379; EMBL:X53011
 C:Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52; ribosome; zinc finger
 C:Keywords: DNA binding; protein biosynthesis; ribosome; zinc finger
 F:1-2/Product: ubiquitin (fragment) #status predicted <UBI>
 F:3-74/Product: ribosomal protein CEP52 #status predicted <RIB>
 F:3-74/Domain: ribosomal protein CEP52 #status predicted <RIB>
 F:22-61/Region: zinc finger CCCC motif
 F:68-74/Region: nuclear location signal

Query Match 24.9%; Score 50; DB 2; Length 74;
 Best Local Similarity 44.4%; Pred. No. 24;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 14 CIPQLRCSNTPPLTCQ 31
 DB 22 CRKCYRCPRRTPTQTCR 39

RESULT 40

T30370

hypothetical protein ORF23 - Lymnaea dispar nuclear polyhedrosis virus
 C:Species: Lymnaea dispar nuclear polyhedrosis virus, LdMNPV
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30370

R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrer, Virgilio 233, 17-34, 1999
 A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymnaea dispar
 A:Reference number: Z20836; MUID:99124785; PMID:9887315
 A:Accession: T30370
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-342 <KUZ>
 A:Cross-references: UNIPROT:Q9YMW1; EMBL:AF081810; PIDN:AAC70208.1

Query Match 24.9%; Score 50; DB 2; Length 342;
 Best Local Similarity 50.0%; Pred. No. 86;
 Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 13 ACIPQLRCSNTPPLTCOR 32

DB 270 ACIRKSRFYKNPILYCSR 289

RESULT 41

C81272

probable aminotransferase (degT family) Cj1294 [imported] - Campylobacter jejuni (strain Probable)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: C81272
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell, Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervirulence
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: C81272
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-376 <PAR>
 A:Cross-references: UNIPROT:Q9PN05; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73721
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj1294
 C:Superfamily: erythromycin resistance protein

QY 1 CSQNEYFDSLHACIPCOL 19

DB 294 CQKEELFESLLHAGIGVQV 312

RESULT 42

GQHU11

tumor necrosis factor receptor 1 precursor [validated] - human
 N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38281; R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
 Genomics 13, 219-224, 1992

QY 1 CSQNEYFDSLHACIPCOL 19

DB 294 CQKEELFESLLHAGIGVQV 312

QY 1 CSQNEYFDSLHACIPCOL 19

DB 294 CQKEELFESLLHAGIGVQV 312

QY 1 CSQNEYFDSLHACIPCOL 19

DB 294 CQKEELFESLLHAGIGVQV 312

RESULT 42

GQHU11

tumor necrosis factor receptor 1 precursor [validated] - human
 N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38281; R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
 Genomics 13, 219-224, 1992
 A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chromosome 6p21
 A:Reference number: A38208; MUID:92250049; PMID:1315717
 A:Accession: A38208
 A:Molecule type: DNA
 A:Residues: 1-455 <FUC>
 A:Cross-references: UNIPROT:P19438; GB:M75864; GB:M75866; NID:g3339748; PIDN:AJR1; Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, Cell 61, 351-359, 1990

QY 1 CSQNEYFDSLHACIPQCLRCSS---NTPPLTCQRYC 34
 Db 499 CRSNEKFE-----PCKTVCSDTKCNBEPFCQVVC 528

RESULT 44
 T27319
 hypothetical protein Y69H2.3b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27319
 R:McMurray, A.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z20343
 A:Accession: T27319
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-626 <WIL>
 A:Cross-references: UNIPROT:Q9U1T5; EMBL:Z98877; PIDN:CAB54473.1; GSPDB:GN00023; CESP:Y69H2
 A:Experimental source: clone Y69H2
 C:Genetics:
 A:Gene: CESP:Y69H2.3b
 A:Map position: 5
 A:Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3

Query Match 24.9%; Score 50; DB 2; Length 626;
 Best Local Similarity 32.4%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

QY 1 CSQNEYFDSLHACIPQCLRCSS---NTPPLTCQRYC 34
 Db 564 CRSNEKFE-----PCKTVCSDTKCNBEPFCQVVC 593

RESULT 45
 T23573
 hypothetical protein K10D3.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T23573
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19762
 A:Accession: T23573
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-922 <WIL>
 A:Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K10D3
 A:Experimental source: clone K10D3
 C:Genetics:
 A:Gene: CESP:K10D3.4
 A:Map position: 1
 A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 24.9%; Score 50; DB 2; Length 922;
 Best Local Similarity 29.3%; Pred. No. 2e+02;
 Matches 12; Conservative 7; Mismatches 14; Indels 8; Gaps 2;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTTPP-----LTCQRY 33
 Db 68 CTQNRQCEAVWPGVCRSGECRCANNQPFTRDGLVCLNY 108

RESULT 46
 F96596
 hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F96596
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96596
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1360 <STO>
 A:Cross-references: UNIPROT:Q9ZVU3; GB:AE005173; NID:g4204269; PIDN:AAD10650.1; GSPDB:GN00023
 C:Genetics:
 A:Gene: T5A14.15
 A:Map position: 1

Query Match 24.9%; Score 50; DB 2; Length 1360;
 Best Local Similarity 50.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 NEYFDSLHACIPQCL 19
 Db 947 NKDTDDLVAACLPCL 962

RESULT 47
 G83398
 Probable two-component sensor PA1979 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: G83398
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: G83398
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-216 <STO>
 A:Cross-references: UNIPROT:Q9I2C8; GB:AE004624; GB:AE004091; NID:g9947973; PIDN:AAG05367
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1979

Query Match 24.6%; Score 49.5; DB 2; Length 216;
 Best Local Similarity 34.3%; Pred. No. 67;
 Matches 12; Conservative 2; Mismatches 12; Indels 9; Gaps 1;

QY 3 QNEYFDSLHAC-----IPCQLRCSSNTTPPL 28
 Db 86 QROSLDEALRACVADWQEGGIACELRLGGPLPPL 120

RESULT 48
 T27303
 hypothetical protein Y68A4.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27303
 R:Steward, C.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20340
 A:Accession: T27303
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-392 <WIL>
 A:Cross-references: UNIPROT:Q9XXP6; EMBL:AL021503; PIDN:CAA16424.1; GSPDB:GN00023; CESP:Y68A4
 A:Experimental source: clone Y68A4
 C:Genetics:
 A:Gene: CESP:Y68A4.10

Search completed: January 28, 2005, 19:57:56
Job time : 9.48624 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:44:33 ; Search time 39.6147 Seconds
(without alignments)
493.825 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201
Sequence: 1 CSQNEVDSLHACIPQLRCSNTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	184	1	TRI17_HUMAN
2	201	100.0	184	2	Q6PE36
3	201	100.0	184	2	AAH58291
4	136	67.7	185	1	TR17_MOUSE
5	72.5	36.1	499	2	Q88714
6	72.5	36.1	1674	2	Q80218
7	72.5	36.1	2850	2	Q80T03
8	71.5	35.6	249	1	TL3X_MOUSE
9	68.5	34.1	1569	2	Q6W4X9
10	68.5	34.1	1569	2	AAQ82434
11	67.5	33.6	1877	1	PCK5_MOUSE
12	66.5	33.1	293	1	TL3X_HUMAN
13	65.5	32.6	1025	2	Q7R607
14	64.5	32.1	5374	2	Q99ND0
15	64.5	32.1	5376	1	ZAN_MOUSE
16	61.5	30.6	3005	2	Q6BFQ4
17	61	30.3	965	2	Q22378
18	60	29.9	867	1	SSFO_BOVIN
19	60	29.9	5146	2	Q8SPM4
20	59.5	29.6	353	2	Q9VW81
21	59.5	29.6	353	2	Q8SZ58
22	59.5	29.6	581	2	Q8NAV8
23	59.5	29.6	880	2	Q8NAV8
24	59.5	29.6	985	2	Q7Z5T8
25	59.5	29.6	985	2	Q8IZ06
26	59.5	29.6	992	2	Q86U29
27	59.5	29.6	993	2	Q8IX30
28	59	29.4	247	2	Q7Z6F5
29	59	29.4	937	2	Q9GYR5
30	58	28.9	101	2	Q8BR19
31	58	28.9	175	1	TL3C_MOUSE

32	58	28.9	175	2	Q8R4W8
33	58	28.9	1299	2	Q26489
34	57.5	28.6	63	1	ICE1_ASCSU
35	57.5	28.6	1679	1	FUR2_DROME
36	57	28.4	321	2	Q9MA00
37	57	28.4	1210	2	Q7R165
38	57	28.4	1717	2	Q26566
39	56.5	28.1	1476	2	Q8WRP4
40	56	27.9	341	2	Q6P233
41	56	27.9	341	2	Q8CPA7
42	56	27.9	341	2	Q9D351
43	56	27.9	341	2	AAH64748
44	56	27.9	387	2	Q9PVD4
45	56	27.9	392	2	Q6NUF1
46	56	27.9	392	2	AAH68640
47	56	27.9	2476	1	ZAN_PIG
48	55.5	27.6	146	2	Q9EP28
49	55.5	27.6	225	2	Q9VE40
50	55.5	27.6	673	2	Q86WK8
51	55.5	27.6	955	2	Q96DN2
52	55.5	27.6	989	2	Q9ZU00
53	55.5	27.6	1084	2	Q6IRM7
54	55.5	27.6	1084	2	AAH70831
55	55.5	27.6	2898	2	Q9VLT6
56	55	27.4	147	1	MSRB_VIBPA
57	55	27.4	330	2	O18118
58	55	27.4	344	2	Q924K7
59	55	27.4	663	2	O81YJ8
60	55	27.4	686	2	Q6POM3
61	55	27.4	686	2	AAH65554
62	55	27.4	724	2	Q6BUV7
63	55	27.4	858	1	TTC7_HUMAN
64	55	27.4	1073	2	Q6QI57
65	55	27.4	1073	2	AAH66242
66	55	27.4	1074	2	Q964D1
67	55	27.4	1101	2	Q964D2
68	55	27.4	1127	2	Q993K9
69	55	27.4	1513	2	O17970
70	54.5	27.1	146	2	Q9EP23
71	54.5	27.1	752	2	Q9C091
72	54.5	27.1	1792	2	O57484
73	54.5	27.1	2155	1	TECA_HUMAN
74	54.5	27.1	2155	1	TECA_MOUSE
75	54	26.9	89	1	VPI_MESMA
76	54	26.9	501	2	Q8WVD2
77	54	26.9	695	2	Q93539
78	54	26.9	718	2	Q9BI07
79	54	26.9	1980	1	MY9B_RAT
80	54	26.9	2114	1	MY9B_MOUSE
81	54	26.9	2158	1	MY9B_HUMAN
82	54	26.9	2447	2	Q9NEF9
83	54	26.9	3215	2	Q8IRV7
84	54	26.9	4117	2	Q8IRV9
85	54	26.9	4179	2	Q9W4Y4
86	54	26.9	4223	2	Q8MRN3
87	54	26.9	4228	2	Q8IRV8
88	53.5	26.6	146	2	Q9EP09
89	53.5	26.6	246	2	Q9TUX4
90	53.5	26.6	281	2	Q29475
91	53.5	26.6	285	2	Q95326
92	53.5	26.6	290	2	Q7Q883
93	53.5	26.6	381	1	P53_CANFA
94	53.5	26.6	414	2	Q68813
95	53.5	26.6	758	1	YJU6_YEAST
96	53.5	26.6	1069	2	Q9BP52
97	53.5	26.6	2843	2	Q9Y6R7
98	53.5	26.6	3084	2	Q7RSL8
99	53	26.4	131	1	ALK1_MOUSE
100	53	26.4	131	2	AAO09307

ALIGNMENTS

RESULT 1
ID TRI7 HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
GN Name=TNFRSF17; Synonyms=BCMA, BCM;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocytes.
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbone F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMBO J. 11:3897-3904 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308 (1999).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
RL Genes Immun. 2:276-279 (2001).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND SER-165.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J.-I., Devergne O., Tsapis A.;
RT "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-activated protein kinase.";
RL J. Immunol. 165:1322-1330 (2000).
RN [7]
RP FUNCTION.
RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.;
RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell autoimmune disease.";
RL Nature 404:995-999 (2000).
RN [8]
RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity.";
RL Nat. Immunol. 1:252-256 (2000).
RN [9]
RP INTERACTIONS WITH TRAF5 AND TRAF6.
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
RA Shu H.-B., Johnson H.;
RT "B cell maturation protein is a receptor for the tumor necrosis factor family member TALL-1";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161 (2000).
CC -!- FUNCTION: Receptor for TNFSF13B/BlyS/BAFF and TNFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-cells or monocytes.
CC -!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia (T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which involves TNFRSF17 and IL2.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC --- SWISS-PROT entry is copyright.. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; Z14954; CAAY78679.1; -
DR EMBL; Z29575; CAAB2691.1; -
DR EMBL; Z29574; CAAB2690.1; -
DR EMBL; U95743; AAB67251.1; -
DR EMBL; AB052772; BAB0895.1; -
DR EMBL; AY509112; AAR84240.1; -
DR PIR; S43486; S43486.
DR PDB; 1ODD; X-ray; K/L/M/N/O/P/Q/R=8-46.
DR Genew; HGNC:11913; TNFRSF17.
DR MIM; 109545; -
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
KW 3D-structure; Chromosomal translocation; Immune response; Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
FT DOMAIN 1 54 Extracellular (Potential).
FT TRANSMEM 55 77 Signal-anchor for type III membrane protein (Potential).
FT DOMAIN 78 184 Cytoplasmic (Potential).
FT REPEAT 7 41 TNFR-Cys.
FT SITE 3 4 Breakpoint for translocation to form IL2/TNFRSF17 oncogene.
FT DISULFID 8 21 By similarity.
FT DISULFID 24 37 By similarity.
FT DISULFID 28 41 By similarity.
FT VARIANT 54 54 A -> V. /FTID=VAR_018755.
FT VARIANT 65 65 I -> V.

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FT VARIANT 75 75 /FTid=VAR_018756.
FT FT -> V.
FT VARIANT 81 81 /FTid=VAR_018757.
FT FT S -> N.
FT VARIANT 153 153 /FTid=VAR_018758.
FT FT A -> T.
FT VARIANT 165 165 /FTid=VAR_012234.
FT FT C -> S.
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 2
Q6PE46 PRELIMINARY; PRT; 184 AA.
AC Q6PE46;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 17.
GN Name=TNFRSF17;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058291; AAH58291.1; -.
KW Receptor.
SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 4
TR17_MOUSE
ID TR17_MOUSE STANDARD; PRT; 185 AA.
AC O88472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN Name=TNFRSF17; Synonyms=BCMA, BCM;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

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gel-forming mucin gene cluster between human and mouse." ;
RT
RL Genomics 81:433-436(2003).
DR EMBL; AY184388; AAC47735.1;
DR EMBL; AY184385; AAC47735.1; JOINED.
DR EMBL; AY184387; AAC47735.1; JOINED.
DR EMBL; AY184386; AAC47735.1; JOINED.
DR HSP; O46162; IKJ0.
DR MGD; MGI:2663233; Muc6.
DR InterPro; IPR002919; Cysrich TIL.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR009041; BMP_SGCI.
DR InterPro; IPR001845; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK 2; 1.
SQ SEQUENCE 2850 AA; 300398 MW; 9CD95F0845C79C9D CRC64;

Query Match 36.1%; Score 72.5; DB 2; Length 2850;
Best Local Similarity 48.3%; Pred. No. 2.3;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 5;

QY 1 CSONEYFDSLHACIPCOLRCSSTNPRLT 29
Db 1222 CSONEYFDHSEGTGVPC-----APPTT 1243

RESULT 8
T13X_MOUSE
ID _T13X_MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Tnfrsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC
RC TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
RT humoral immunity." ;
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354693; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,
RA Grimmmond S., Gustinchin S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Portea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

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Query Match 34.1%; Score 68.5; DB 2; Length 1569;
 Best Local Similarity 45.2%; Pred. No. 4.1;
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 1 CSQNEYPDLSLLHACIPQCLRSSNTPTLTCQ 31
 DB_ 1179 CSQNEYPDHEGVCVPCM-----PPTTPQ 1202

RESULT 11

ID_PCK5 MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q62040; PRT; 1877 AA.

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

DE (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)

DE (Subtilisin-like proprotein convertase 6) (SPC6).

GN Name=PC5K5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).

RC STRAIN=ICR; TISSUE=Intestine;

RX MEDLINE=93327934; PubMed=8335106;

RA Nakagawa T., Murakami K., Nakayama K.;

RT "Identification of an isoform with an extremely large Cys-rich region
 of PC5, a Kex2-like processing endoprotease.";

RL FEBS Lett. 327:165-171 (1993).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Brain, and Intestine;

RX MEDLINE=93224489; PubMed=8468318;

RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;

RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";

RL J. Biochem. 113:132-135 (1993).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Adrenal cortex;

RX MEDLINE=93342056; PubMed=8341687;

RA Lussan J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;

RT "CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]

RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.

RX MEDLINE=97103178; PubMed=8947550;

RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bhandaryan M., Seidah N.G.;

RT "The isoforms of proprotein convertase PC5 are sorted to different
 subcellular compartments.";

RL J. Cell Biol. 135:1261-1275 (1996).

RN [5]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=96293359; PubMed=8698813;

RA Constam D.B., Calton M., Robertson E.J.;

RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";

RL J. Cell Biol. 134:181-191 (1996).

RN [6]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=97436919; PubMed=9291583;

RA Rancourt S.L., Rancourt D.E.;

RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";

RL Dev. Genet. 21:75-81 (1997).

CC -!- FUNCTION: Likely to represent a widespread endoprotease activity
 within the constitutive and regulated secretory pathway. Capable
 of cleavage at the RX(K/R)R consensus motif. May be responsible
 for the maturation of gastrointestinal peptides. May be involved
 in the cellular proliferation of adrenal cortex via the activation
 of growth factors.

CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 can be any amino acid and Yaa is Arg or Lys.

CC -!- SUBCELLULAR LOCATION: PC5A is secreted through the regulated
 secretory pathway. PC5B is a type I membrane protein localized to
 a paranuclear post-Golgi network compartment in communication with
 early endosomes.

CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=PC5B; Synonyms=Long;
 IsoId=Q04592-1; Sequence=Displayed;
 Name=PC5A; Synonyms=Short;
 IsoId=Q04592-2; Sequence=VSP_005438, VSP_005439;

CC -!- TISSUE SPECIFICITY: PC5A is expressed in most tissues but is most
 abundant in the intestine and adrenals. PC5B is expressed in the
 intestine, adrenals and lung but not in the brain.

CC -!- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo,
 except in the developing nervous system, the ribs and the liver,
 but markedly up-regulated at discrete sites during development. At
 E6.5, prominent expression observed in differentiated decidua. At
 E7.5, intense expression in extraembryonic endoderm, amnion and
 nascent mesoderm. At E8.5, abundant expression in somites and yolk
 sac followed by a confinement to dermomyotome compartment. Between
 E9.5 and E11.5, abundant expression in AER (thickened ectodermal
 cells of limb buds). At E12.5, expression in the limbs is confined
 to the condensing mesenchym surrounding the cartilage. At this
 stage, strong expression also detected in vertebral and facial
 cartilage primordia and in the muscle of the tongue. At E16.5,
 abundant expression in epithelial cells of the intestinal villi.
 Isoform A is most abundant at all stages but significant levels of
 isoform B occur at E12.5.

CC -!- DOMAIN: The propeptide domain acts as an intramolecular chaperone
 assisting the folding of the zymogen within the endoplasmic
 reticulum.

CC -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
 sorting information. AC 1 directs TGN localization and interacts
 with the TGN sorting protein PACS-1.

CC -!- SIMILARITY: Belongs to peptidase family S8.

CC -!- SIMILARITY: Contains 1 homo B/P domain.

CC -----

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 or send an email to license@isb-sib.ch).

CC -----

CC EMBL; D17583; BAA04507.1; -
 CC EMBL; D12619; BAA02143.1; -
 CC EMBL; L14932; AAA74636.1; -
 CC PIR; A48225; A48225
 CC PIR; A34583; S34583.
 CC HSP; P23188; IP8U.
 CC MEROPS; S08.076; -
 CC MG; MG1.97515; Pcsk5.
 CC InterPro; IPR006211; Furin-like.
 CC InterPro; IPR009030; Grow_fac_recept.
 CC InterPro; IPR011031; MultThaem_cyt.
 CC InterPro; IPR000209; Pept_S8_S53.
 CC InterPro; IPR002884; Protnconvertsp.
 CC Pfam; PF00757; Furin-like; 2.
 CC Pfam; PF00082; Peptidase S8; 1.
 CC Pfam; PF01483; P_protein; 1.
 CC PRINTS; PR00723; SUBTILISIN.


```
QY 1 CSQNEYFDSLLHACIP-COLRGSSNTP--PLTCQRYC 34
Db 3298 CPTNSQFTDCLPSCVPCSNRCVTSVPSSCREG 3334

RESULT 15
ZAN MOUSE
ID ZAN MOUSE STANDARD; PRT; 5376 AA.
AC O88799; O08647;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Zonadhesin precursor.
GN Name=Zan;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98123114; PubMed=9452463;
RA Gao Z., Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RT domains."
RL J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z., Harumi T., Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
RT zonadhesin gene (ZAN)."
RL Genomics 41:119-122(1997).
CC -!- FUNCTION: Binds in a species-specific manner to the zona pellucida
CC of the egg. May be involved in gamete recognition and/or
CC signaling.
CC -!- SUBUNIT: Probably forms covalent oligomers.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the
CC apical region of the sperm head.
CC -!- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.
CC -!- DOMAIN: The NAM domains probably mediates sperm adhesion to the
CC zona pellucida.
CC -!- DOMAIN: During sperm migration through the reproductive tracts,
CC the mucin-like domain might inhibit inappropriate trapping of
CC spermatozoa or promoting adhesion to the oviductal isthmus.
CC -!- DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By
CC similarity).
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 3 NAM domains.
CC -!- SIMILARITY: Contains 25 VWFD domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U97068; AAC26680.1; -
CC EMBL; U83190; AAC53125.1; -
CC PIR; T42215; T42215.
CC HSSP; Q90248; 1HX2.
CC MGD; MGI:106656; Zan.
CC InterPro; IPR002919; Cysrich_TIL.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR000998; NAM.
CC InterPro; IPR003328; TILA Cysrich.
CC InterPro; IPR001846; VWF_D.

DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TIL_assoc; 25.
DR Pfam; PF00094; VWD; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00740; MAM_1; FALSE_NEG.
DR PROSITE; PS00060; MAM_2; 3.
KW Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 5376 Zonadhesin.
FT DOMAIN 18 5310 Extracellular (Potential).
FT TRANSEM 5311 5337 Potential.
FT DOMAIN 5338 5376 Cytoplasmic (Potential).
FT DOMAIN 45 210 MAM 1.
FT DOMAIN 215 374 MAM 2.
FT DOMAIN 377 542 MAM 3.
FT DOMAIN 547 1170 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
FT (MUCIN-LIKE DOMAIN).
FT DOMAIN 1171 1280 VWFD 1 (partial).
FT DOMAIN 1281 1669 VWFD 2.
FT DOMAIN 1670 2056 VWFD 3.
FT DOMAIN 2057 2459 VWFD 4.
FT DOMAIN 2460 2579 VWFD 5 (partial).
FT DOMAIN 2580 2699 VWFD 6 (partial).
FT DOMAIN 2700 2819 VWFD 7 (partial).
FT DOMAIN 2820 2939 VWFD 8 (partial).
FT DOMAIN 2940 3059 VWFD 9 (partial).
FT DOMAIN 3060 3179 VWFD 10 (partial).
FT DOMAIN 3180 3299 VWFD 11 (partial).
FT DOMAIN 3300 3416 VWFD 12 (partial).
FT DOMAIN 3417 3536 VWFD 13 (partial).
FT DOMAIN 3537 3656 VWFD 14 (partial).
FT DOMAIN 3657 3776 VWFD 15 (partial).
FT DOMAIN 3777 3892 VWFD 16 (partial).
FT DOMAIN 3893 4928 VWFD 17 (partial).
FT DOMAIN 4029 4148 VWFD 18 (partial).
FT DOMAIN 4149 4263 VWFD 19 (partial).
FT DOMAIN 4264 4283 VWFD 20 (partial).
FT DOMAIN 4384 4503 VWFD 21 (partial).
FT DOMAIN 4504 4623 VWFD 22 (partial).
FT DOMAIN 4624 4743 VWFD 23 (partial).
FT DOMAIN 4744 4863 VWFD 24 (partial).
FT DOMAIN 4864 5261 VWFD 25.
FT DOMAIN 5259 5295 EGF-like.
FT DISULFID 5263 5274 By similarity.
FT DISULFID 5268 5283 By similarity.
FT DISULFID 5285 5294 By similarity.
FT CARBOHYD 339 339 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 499 499 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1216 1216 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1239 1239 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1314 1314 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1814 1814 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1908 1908 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1933 1933 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2028 2028 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2111 2111 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2142 2142 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2332 2332 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2533 2533 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2575 2575 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2692 2692 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 2812 2812 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3052 3052 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3065 3065 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3144 3144 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3172 3172 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3288 3288 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 3292 3292 N-linked (GlcNAc. .) (Potential).
```

FT CARBOHYD 3782 3782 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4005 4005 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4136 4136 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4243 4243 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4254 4254 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4335 4335 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4376 4376 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4586 4586 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 5136 5136 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 5252 5252 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB7DF2A2620 CRC64;

Query Match 32.1%; Score 64.5; DB 1; Length 5376;
 Best Local Similarity 35.1%; Pred. No. 50;
 Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Oy 1 CSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 34
 Db 3300 CPTNSQFTDCLPSCVPSNCEVTSPSPVSCREGC 3336

RESULT 16

Q6BFG4 PRELIMINARY; PRT; 3005 AA.
 AC Q6BFG4;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Putative surface protein with EGF domains and furin-like repeats.
 GN ORFNames=PTMB.409;
 OS Paramesicium tetraurelia.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramesicium.
 OX NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stock d4-2;
 RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
 RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
 RA Cohen J., Meyer E., Sperling L.;
 RT "High coding density on the largest Paramesicium tetraurelia somatic
 chromosome."
 RL Curr. Biol. 0:0-0(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stock d4-2;
 RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR548612; CAH03606.1; -;
 SQ SEQUENCE 3005 AA; 343821 MW; D8CC6A247876A5A5 CRC64;

Query Match 30.6%; Score 61.5; DB 2; Length 3005;
 Best Local Similarity 40.6%; Pred. No. 68;
 Matches 13; Conservative 3; Mismatches 7; Indels 9; Gaps 2;

Oy 6 YFDSLHACIPQCLRCSTNTPPLTCQ---RYC 34
 Db 1190 YFESSTNQICDLSC-----FTCGSSKYC 1215

RESULT 17

ID Q22378 PRELIMINARY; PRT; 966 AA.
 AC Q22378;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein T10E10.4.
 GN ORFNames=T10E10.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Geisel C.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U39644; AAA80360.2; -;
 DR PIR; T16840; T16840.
 DR HSSP; P10969; LWGT.
 DR WormPep; T10E10.4; CE25989.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR InterPro; IPR002557; Chitin_bind_Pera.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR003571; Snake toxin.
 DR InterPro; IPR000794; Ketoacyl synth.
 DR InterPro; IPR006150; Worm_repeat_1.
 DR Pfam; PF01607; CBM_14; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00289; WRI; 12.
 DR PROSITE; PS00606; B_KETOACYL SYNTHASE; UNKNOWN_1.
 DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;

Query Match 30.3%; Score 61; DB 2; Length 966;
 Best Local Similarity 37.5%; Pred. No. 24;
 Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSQNEYFDSLHACIPQCLR--CSSNTPPLTC 30
 Db 216 CSQSTVFNSDLNVCVPLAIQNSCDSDSTQQPVC 247

RESULT 18

SSPO_BOVIN
 ID SSPO_BOVIN STANDARD; PRT; 867 AA.
 AC P98167;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE SCO-spondin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ependymocyte;
 RX MEDLINE=96338614; PubMed=8743952;
 RA Gobron S., Monnerie H., Meiniet R., Creveaux I., Lehmann W.,
 RA Lamalle D., Dastugue B., Meiniet A.;
 RT "SCO-spondin: a new member of the thrombospondin family secreted by
 the subcommissural organ is a candidate in the modulation of neuronal

RT aggregation.";

RL J. Cell Sci. 109:1053-1061(1996).

CC -!- FUNCTION: Involved in the modulation of neuronal aggregation.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Subcommissural organ.

CC -!- DEVELOPMENTAL STAGE: Embryo.

CC -!- SIMILARITY: Belongs to the thrombospondin family.

CC -!- SIMILARITY: Contains at least 2 EGF-like domains.

CC -!- SIMILARITY: Contains at least 1 F5/F8 type C domain.

CC -!- SIMILARITY: Contains at least 1 F5/F8 type C domain.

CC -!- SIMILARITY: Contains at least 3 LDL-receptor class A domains.

CC -!- SIMILARITY: Contains at least 4 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 VWFC domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X93922; CAA63815.1; --

DR HSP; P01130; LAJU.

DR InterPro; IPR002919; Cysrich_TIL.

DR InterPro; IPR000421; FAS8_C.

DR InterPro; IPR008979; Gal_Bind like.

DR InterPro; IPR002172; LDL receptor_A.

DR InterPro; IPR009041; PMP_SGCI.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR001007; VWFC_C.

DR Pfam; PF00754; F5_F8_type_C; 1.

DR Pfam; PF00057; Ldl_recept_a; 3.

DR Pfam; PF01826; TIL; 1.

DR Pfam; PF00090; TSP_1; 4.

DR Pfam; PF00093; VWC_1.

DR PRINTS; PRO0261; LDLRECEPTOR.

DR PRINTS; PRO1705; TSP1REPEAT.

DR PROSITE; PS01285; FA58C_1; 1.

DR PROSITE; PS01286; FA58C_2; 1.

DR PROSITE; PS00022; FA58C_3; 1.

DR PROSITE; PS01209; LDLRA_1; 3.

DR PROSITE; PS00068; LDLRA_2; 3.

DR PROSITE; PS00092; TSP1; 4.

DR PROSITE; PS0184; VWFC_2; 1.

DR Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.

FT NON_TER 1

FT DOMAIN 1

FT DOMAIN 29 87 TSP type-1 1.

FT DOMAIN 103 142 EGF-like 1.

FT DOMAIN 143 180 EGF-like 2.

FT DOMAIN 188 244 TSP type-1 2.

FT DOMAIN 245 304 VWFC.

FT DOMAIN 344 502 F5/F8 type C.

FT DOMAIN 506 544 LDL-receptor class A 1.

FT DOMAIN 663 701 LDL-receptor class A 2.

FT DOMAIN 723 761 LDL-receptor class A 3.

FT DOMAIN 761 814 TSP type-1 3.

FT DOMAIN 816 866 TSP type-1 4.

FT DISULFID 107 122 By similarity.

FT DISULFID 116 127 By similarity.

FT DISULFID 129 141 By similarity.

FT DISULFID 147 166 By similarity.

FT DISULFID 149 169 By similarity.

FT DISULFID 171 179 By similarity.

FT DISULFID 344 502 By similarity.

FT DISULFID 508 520 By similarity.

FT DISULFID 515 533 By similarity.

FT DISULFID 527 542 By similarity.

FT DISULFID 665 677 By similarity.

FT DISULFID 672 690 By similarity.

FT DISULFID 684 699 By similarity.

FT DISULFID 725 737 By similarity.

FT DISULFID 732 750 By similarity.

FT DISULFID 744 759 By similarity.

FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 409 409 N-linked (GlcNAc...) (Potential).

FT NON_TER 867 867

SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match 29, 98; Score 60; DB 1; Length 867;

Best Local Similarity 42.9%; Pred. No. 29;

Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 10 LHHACIPQCQLRCSSNTPLTLC 30

Db 96 VFHACVCPCLTCDISQATC 116

RESULT 19

Q8SPM4 PRELIMINARY; PRT; 5146 AA.

AC Q8SPM4;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE SCO-spondin.

GN Name=sco-spondin;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Subcommissural organ;

RX MEDLINE=20465125; PubMed=11008217;

RA Gobron S.;

RT "Subcommissural organ/Reissner's fiber complex: characterization of

RT SCO-spondin, a glycoprotein with potent activity on neurite

RT outgrowth.";

RL Glia 32:177-191(2000).

RZ [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Subcommissural organ;

RA Meinzel A.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416457; CAC94914.1; --

DR HSP; P98162; IK7B.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR GO; GO:0030414; F:protease inhibitor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR002919; Cysrich_TIL.

DR InterPro; IPR006207; Cys_knot_C.

DR InterPro; IPR011489; EMI.

DR InterPro; IPR000421; FAS8_C.

DR InterPro; IPR001545; Gly_hormoneB.

DR InterPro; IPR002172; LDL_receptor_A.

DR InterPro; IPR009041; PMP_SGCI.

DR InterPro; IPR008037; PMP_inh_PMP.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR001007; VWFC_C.

DR InterPro; IPR001846; VWFC_D.

DR Pfam; PF07546; EMI; 1.

DR Pfam; PF00754; F5_F8_type_C; 1.

DR Pfam; PF00057; Ldl_recept_a; 10.

DR Pfam; PF05375; Pacifastin_I; 1.

DR Pfam; PF01826; TIL; 10.

DR Pfam; PF00090; TSP_1; 25.

DR Pfam; PF00093; VWC; 1.

DR Pfam; PF00094; VWD; 3.

DR PRINTS; PRO0261; LDLRECEPTOR.

DR SMART; SM00041; CT; 1.

DR SMART; SM00231; FA58C; 1.

DR SMART; SM00068; GHB; 1.

Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*"; Science 287:2195-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleab J.M., Park S., Pfeiffer B.D., Richards M., Sodergren E.J., Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila melanogaster* euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradycky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktarglu L., Bertram B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN SEQUENCE FROM N.A.
RP SUBMITTED (SEP-2002) TO THE EMBL/GenBank/DBJ DATABASES.
[6]
RN SEQUENCE FROM N.A.
RP FLYBASE;
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE FROM N.A.
RP FLYBASE;
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003514; AAFA9068.1; -;
DR FlyBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR Pfam; PF01607; CBM_14; 4.
DR SMART; SM00494; CHTBD2_3.
DR PROSITE; PS00940; CHIT_BIND II; 4.
SQ SEQUENCE 353 AA; 39713 MW; 1C66916504FDI30B CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. NO. 13;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps

Qy 1 CSONEYFDSLHACIPCOL-----RCSSNTP-----PLTCORY 33
Db 119 CSVGNFYDPARRACLPAISAHAQCVCVLPDNATLANPSDCETY 162

RESULT 21
Q8SZ58 PRELIMINARY; PRT; 353 AA.
ID Q8SZ58
AC Q8SZ58

DR	SMART; SM00192; LDla; 10.
DR	SMART; SM00209; TSPI; 25.
DR	SMART; SM00214; WVC; 3.
DR	SMART; SM00216; VWD; 3.
DR	PROSITE; PS01225; CTCK_2; 1.
DR	PROSITE; PS01285; FA58C_1; UNKNOWN_1.
DR	PROSITE; PS01286; FA58C_2; 1.
DR	PROSITE; PS00022; FA58C_3; 1.
DR	PROSITE; PS00261; GLYCO HORMONE_BETA_1; 2.
DR	PROSITE; PS01209; LDLRA_1; 7.
DR	PROSITE; PS00068; LDLRA_2; 9.
DR	PROSITE; PS00092; TSPL_25.
DR	PROSITE; PS01208; VFPC_1; UNKNOWN_1.
DR	PROSITE; PS00184; VWFC_2; 2.
SQ	SEQUENCE 5146 AA; 54358 MW; 724C5FB877E13DA CRC64;
Query Match	29.9%; Score 60; DB 2; Length 5146;
Best Local Similarity	42.9%; Pred. No. 1.9e+02;
Matches	9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Oy	10 LHACIPCOLRCSSNTPPLTC 30
Db	1814 VFHACVCPCLTCDDBDISQATC 1834
RESULT 20	
Q9VM81	PRELIMINARY; PRT; 353 AA.
ID	Q9VM81
AC	Q9VM81
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN	Cg7348-PA.
DE	ORFNames=Cg7348;
OS	Drosophila melanogaster (fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Mortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gaber G.L.,
RA	Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Purbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA	Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwa C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lauko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nueskern D.R., Paclel J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang M., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster.";
RL	Science 287:2185-2195(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22426065; PubMed=12537568;
RA	Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA	Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA	George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA	Paclel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA	Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA	Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT	"Finishing a whole-genome shotgun: release 3 of the Drosophila
RT	melanogaster euchromatic genome sequence.";
RL	Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22426070; PubMed=12537573;
RA	Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA	Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA	Ashburner M., Celniker S.E.;
RT	"The transposable elements of the Drosophila melanogaster euchromatin:
RT	a genomics perspective.";
RL	Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22426069; PubMed=12537572;
RA	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA	Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA	Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA	Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA	Lewis S.E.;
RT	"Annotation of the Drosophila melanogaster euchromatic genome: a
RT	systematic review.";
RL	Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN	[5]
RP	SEQUENCE FROM N.A.
RG	FLYBASE;
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN	[6]
RP	SEQUENCE FROM N.A.
RG	FLYBASE;
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AE003514; AAF49068.1; -
DR	FlyBase; FBgn0036940; CG7348.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0008061; P:chitin binding; IEA.
DR	GO; GO:0006030; P:chitin metabolism; IEA.
DR	InferPro; IPR002557; Chitin_bind_PerA.
DR	Pfam; PF01607; CBM_14; 4.
DR	SMART; SM00494; CHTB2D_3.
DR	PROSITE; PS00940; CHIT_BIND II; 4.

DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE RE16222p.
 GN ORFName=CG7348;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY071103; AAL48725.1; -;
 DR FLYBase; FBgn0036940; CG7348.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0006030; F:chitin metabolism; IEA.
 DR InterPro; IPR002557; Chitin_bind_PerA.
 DR Pfam; PF01607; CBM 14; 4.
 DR SMART; SM00494; ChitBD2; 3.
 DR PROSITE; PS05940; CHIT_BIND II; 4.
 SQ SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

 Query Match 29.6%; Score 59.5; DB 2; Length 353;
 Best Local Similarity 31.8%; Pred. No. 13;
 Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

 QY 1 CSQNEYPDSLHACIPCOL-----RCSNTP-----PLTCQRY 33
 DB 119 CSVGNFDPARRACLPFAISAHQCSVLFPDNLANPSCDCTY 162

 RESULT 22
 Q8NAV8
 ID Q8NAV8 PRELIMINARY; PRT; 581 AA.
 AC Q8NAV8;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ34691.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 EX PubMed=14702039;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Tanai H., Hosoiri T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Murakami K., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata S., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata S., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata S., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togoashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK092010; BAC03789.1; -;
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDALIE4BE1 CRC64;

 Query Match 29.6%; Score 59.5; DB 2; Length 581;
 Best Local Similarity 28.9%; Pred. No. 22;
 Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

 QY 1 CSQNEYPDSLHACIPCOL-----RCSNNT 25
 DB 337 CSPGHYNTSIHRCIRCMGSIQDFRQNFSCRCPGNT 374

 RESULT 23
 Q8NAU9
 ID Q8NAU9 PRELIMINARY; PRT; 880 AA.
 AC Q8NAU9;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ34743.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata S., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata S., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Best Local Similarity 28.3%; Pred. No. 39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEVFDLLHACIPCQL-----RCSNNT 25
Db 748 CSRGHYVTSIHRCCAMGSYDPFRNFCSCPGNT 785

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RESULT 27
QBIX30          QBIX30
ID              PRELIMINARY;      PRT;    993 AA.
AC              QBIX30;
DT              01-WAR-2003 (TReMBLrel. 23, Created)
DT              01-WAR-2003 (TReMBLrel. 23, Last sequence update)
DE              01-WAR-2004 (TReMBLrel. 26, Last annotation update)
DE              CUB and EGF containing protein.
DN              Name=CEGF3;
OS              Homo sapiens (Human).
OC              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX              NCBI_TaxID=9606;
RN              [1]
SEQUENCE FROM N.A.
RP              Pfaffr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt
RA              Hankeln T., Winterpacht A.;
RL              Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR              EMBL; AF452494; AAN76808.1; -.
DR              HSSP; F35555; IENN.
DR              GO; GO:0005509; F:calcium ion binding; IEA.
DR              InterPro; IPRO00152; Asx hydroxyl_S.
DR              InterPro; IPRO00859; CUB_2.
DR              InterPro; IPRO00742; EGF_2.
DR              InterPro; IPRO01881; EGF_Ca.
DR              InterPro; IPRO06209; EGF_like.
DR              InterPro; IPRO09030; Grow_fac_recept.
DR              Pfam; PF00431; CUB; 1.
DR              Pfam; PF00008; EGF; 4.
DR              Pfam; PF07645; EGF_CA; 4.
DR              SMART; SM00042; CUB; 1.
DR              SMART; SM00179; EGF CA; 6.
DR              PROSITE; PS00010; ASX_HYDROXYL; 6.
DR              PROSITE; PS01180; CUB; 1.
DR              PROSITE; PS01186; EGF_2; 7.
DR              PROSITE; PS50026; EGF_3; 5.
DR              PROSITE; PS01187; EGF_CA; 6.
DR              EGF-like domain.
SQ              SEQUENCE 993 AA; 109282 MW; 19BBE0E5627BEAF4 CRC64;
KW
Query Match                29.6%; Score 59.5; DB 2; Length 993;
Best Local Similarity     28.9%; Pred.No.39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 13;

QY      1 CSONEYFDSLHACTPCQL-----RCSNST 25
           |||:::|||::|||::|||
DB      749 CSPGHYYNTSIHRCIRCAGSYQPDPFRQNFCSCPGNT 786

RESULT 28
Q7Z6F5          Q7Z6F5
ID              PRELIMINARY;      PRT;    247 AA.
AC              Q7Z6F5;
DT              01-OCT-2003 (TReMBLrel. 25, Created)
DT              01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE              01-WAR-2004 (TReMBLrel. 26, Last annotation update)
DE              Transmembrane activator and CAML interactor.
DN              Name=TNFRSF13B;
OS              Homo sapiens (Human).
OC              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX              NCBI_TaxID=9606;
RN              [1]
SEQUENCE FROM N.A.
RP              Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RA              Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;

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RP
SEQUENCE FROM N.A.
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY302137; AAP57629.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578E8E6 CRC64;

Query Match 29.4%; Score 59; DB 2; Length 247;
 Best Local Similarity 34.4%; Pred. No. 11;
 Matches 11; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

OY 3 QNEVFDLSLHACIPCLRCSSNTPTLTQRYC 34
 DB 29 QGKYDHLRLDCISCASICGGH--PKQAYFC 58

RESULT 29

O9GVR5 PRELIMINARY; PRT; 937 AA.
 ID O9GVR5
 AC O9GVR5
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein C23G10.8.
 GN ORFNames=C23G10.8;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

Query Match 29.4%; Score 59; DB 2; Length 937;
 Best Local Similarity 42.9%; Pred. No. 43;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 8 DSLHACIPCLRCSSNTPTLT 28
 DB 439 ESVFHPYLPATIRCSADGPPL 459

RESULT 30

O8BR19 PRELIMINARY; PRT; 101 AA.
 ID O8BR19
 AC O8BR19
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
 DE enriched library, clone:B230316E19 product:hypothetical protein, full
 DE insert sequence.

OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Higaoka I., Kasukawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kigawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK045875; BAC32518.1; -.
 KW Hypothetical protein.

SQ SEQUENCE 101 AA; 11571 MW; E899420B6F215D23 CRC64;

Query Match 28.9%; Score 58; DB 2; Length 101;
 Best Local Similarity 31.9%; Pred. No. 5.7;
 Matches 15; Conservative 5; Mismatches 9; Indels 18; Gaps 2;

OY 6 YFDSLHACIPC-----QLRCSSNTPTT-----LTCQRYC 34

RN SEQUENCE FROM N.A.
 RA Mizuno K., Irie S., Sato T.-A.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF350257; AAL83914.1; -;
 DR HSP; Q96R33; LOOE.
 DR MGD; MGI:1919299; Tnfrsf13c.
 SQ SEQUENCE 175 AA; 18846 MW; B64EFF4B52EB93B1 CRC64;

Query Match 28.9%; Score 58; DB 2; Length 175;
 Best Local Similarity 47.4%; Pred. No. 10;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOL 19
 Db 22 CQNETCEDPLVRNCVSEL 40

RESULT 33

Q26489 PRELIMINARY; PRT; 1299 AA.
 AC Q26489;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Endoprotease FURIN.
 GN Name=FURIN;
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SF9;
 RA Clepik M., Klenk H.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S8.
 DR EMBL; Z68888; CAA93116.1; -;
 DR PIR; T43251; T43251.
 DR HSP; P23188; 1P8J.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
 DR InterPro; IPR00345; CytC heme BS.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow Fac. recept.
 DR InterPro; IPR011031; Multiheme_cyt.
 DR InterPro; IPR000209; Pept S8_S53.
 DR InterPro; IPR009020; Prot inh proteopt.
 DR InterPro; IPR002884; Proteinconvertsp.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF01483; P_protein; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00190; CVTCHROME C; UNKNOWN 3.
 DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 1299 AA; 142019 MW; 4C3799C7B8C572AB CRC64;

Query Match 28.9%; Score 58; DB 2; Length 1299;
 Best Local Similarity 37.1%; Pred. No. 82;
 Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

Qy 1 CSQNEYFDSLHACIPCOLRCS-----SNTPLPLTC 30
 Db 1150 CSRPLRIDRLNNQCVPC---CSERGVTNSTPTDC 1181

RESULT 34

ICE1_ASCSU STANDARD; PRT; 63 AA.
 AC P07851; O77419;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Chymotrypsin/elastase isoform 1 (C/E-1 inhibitor) (ASC/E-1).
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R., Peanasky R.J., Goos S.M.;
 RT "The isoform 1 of chymotrypsin/elastase from Ascaris lumbricoidea:
 the primary structure.";
 RL Arch. Biochem. Biophys. 232:143-161(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98297373; PubMed=9635450;
 RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
 RT "Aniakas simplex: mutational bursts in the reactive site centers of
 serine protease inhibitors from an ascarid nematode.";
 RL Exp. Parasitol. 89:257-261(1998).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
 RX MEDLINE=95006335; PubMed=7922044;
 RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
 RT "The molecular structure of the complex of Ascaris
 chymotrypsin/elastase inhibitor with porcine elastase.";
 RL Structure 2:679-689(1994).
 CC -1- FUNCTION: Defends the organism against the host's proteinases.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; U94499; AAC61300.1; -;
 CC PDB; 1EAI; X-ray; C/D=1-61.
 DR InterPro; IPR002919; Cysrich_TIL.
 DR Pfam; PF01826; TIL; 1.
 KW 3D-structure; Direct protein sequencing; Serine protease inhibitor.
 FT DOMAIN 5 60
 FT SITE 31 32
 FT DISULFID 5 38
 FT DISULFID 14 33
 FT DISULFID 17 29
 FT DISULFID 21 60
 FT DISULFID 40 54
 FT CONFLICT 4 4
 FT CONFLICT 23 24
 FT TURN 3 4
 FT TURN 7 8
 FT STRAND 10 12
 FT STRAND 15 15
 FT STRAND 20 20
 FT TURN 25 26
 FT STRAND 28 30
 FT STRAND 34 34
 FT STRAND 37 39
 S -> R (in Ref. 2).
 PD -> DP (in Ref. 2).

DR EMBL; L33831; AAA69860.1; -.
 DR EMBL; AB003502; AAF48598.2; -.
 DR EMBL; AB003502; AAF48598.2; -.
 DR EMBL; AY070553; AAL48024.1; ALT_INIT.
 DR PIR; A43434; A43434.
 DR HSSP; P23188; 1P8J.
 DR MEROPS; S08.049; -.
 DR Flybase; FBgn0004598; Fur2.
 DR GO; GO:0004276; F:furin activity; IDA.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR011031; Multihem cyt..
 DR InterPro; IPR000209; Rept_S8_S53.
 DR InterPro; IPR009020; Prot_inh_propept.
 DR InterPro; IPR002884; Pprtnconvertsp.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF01483; P_protein; 2.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 DR Repeat; Repeat: Serine protease; Signal; Transmembrane; Zymogen.
 FT SIGNAL 1 ? Potential.
 FT PROPEP 318 Potential.
 FT CHAIN 319 1679 Furin-like protease 2.
 FT ACT_SITE 417 417 Charge relay system (By similarity).
 FT ACT_SITE 456 456 Charge relay system (By similarity).
 FT ACT_SITE 637 637 Charge relay system (By similarity).
 FT DOMAIN 961 1443 10 X tandem repeats, Cys-rich.
 FT REPEAT 961 1006 1.
 FT REPEAT 1007 1056 2.
 FT REPEAT 1057 1103 3.
 FT REPEAT 1104 1152 4.
 FT REPEAT 1153 1204 5.
 FT REPEAT 1205 1253 6.
 FT REPEAT 1254 1298 7.
 FT REPEAT 1299 1345 8.
 FT REPEAT 1346 1392 9.
 FT REPEAT 1393 1443 10.
 FT TRANSMEM 1512 1532 Potential.
 FT DOMAIN 1533 1679 Cytoplasmic (Potential).
 FT DISULFID 473 629 By similarity.
 FT DISULFID 565 595 By similarity.
 FT DISULFID 720 748 By similarity.
 FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 442 442 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 927 927 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1060 1060 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1181 1181 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1274 1274 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1277 1277 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1439 1439 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 386 386 L -> LVSK (in isoform A).
 FT FTid-VSP 009365.
 FT MISSING (in Ref. 1).
 FT CONFLICT 152 153 Missing (in Ref. 1).
 FT CONFLICT 177 177 V -> F (in Ref. 1).
 FT CONFLICT 213 213 V -> VDQL (in Ref. 1).
 SQ SEQUENCE 1679 AA; 183369 MW; 3F9E749F0B021CF6 CRC64;
 Query Match 28.6%; Score 57.5; DB 1; Length 1679;
 Best Local Similarity 34.3%; Pred. No. 1.2e+02;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSS-NTEPLTCQRYC 34
 Db 1198 CSESEFYQVEGQCRPCHASGSCNGPADTSC 1232
 RESULT 36
 Q9MAMO PRELIMINARY; PRT; 321 AA.
 AC Q9MAMO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T25K16.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
 RA Theologis A., Ecker J.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 Myb-like domain.
 DR EMBL; AC007323; AAF26467.1; -.
 DR HSSP; P54274; IITY.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR011011; FYVE PHD Znf.
 DR InterPro; IPR009057; Homeodomain like.
 DR InterPro; IPR001005; Myb_DNA_binding.
 DR InterPro; IPR001965; Znf_PHD.
 DR SMART; SM00717; SANT; 1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS50090; MYB_3; 1.
 DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
 KW Nuclear protein.
 SQ SEQUENCE 321 AA; 36643 MW; F3411A75DBC0B406 CRC64;
 Query Match 28.4%; Score 57; DB 2; Length 321;
 Best Local Similarity 41.4%; Pred. No. 26;
 Matches 12; Conservative 1; Mismatches 10; Indels 6; Gaps 1;
 Qy 12 HACIPQLR-----CSSNTPPLTCQRYC 34
 Db 63 HACTVCDIADGGVVPVCSGNECLAVHRKC 91
 RESULT 37
 Q7R165 PRELIMINARY; PRT; 1210 AA.
 AC Q7R165;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP_447_61408_57776.

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OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACB0100029; EAA41074.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 23
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 2.
KW ANK repeat.
SQ SEQUENCE 1210 AA; 132500 MW; 0AC83EBA78A5D726 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1210;
Best Local Similarity 35.7%; Pred. No. 1e+02;
Matches 15; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

QY 1 CSQNEYFDSLHLH-----ACIPQ-----QLRCSSNTPL 28
DB 549 CIRNNGTALHIAVASKFACIPCLAAVEARIDSHNRNAL 590

RESULT 38
Q26566
ID Q26566 PRELIMINARY; PRT; 1717 AA.
AC Q26566;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epidermal growth factor receptor precursor.
GN Name=SER;
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=9236572; PubMed=1501637;
RA Shoemaker C.B., Ramchandran H., Landa A., dos Reis M.G., Stein L.;
RT "Alternative splicing of the Schistosoma mansoni gene encoding a
RL homologue of epidermal growth factor receptor.";
RL Mol. Biochem. Parasitol. 53:17-32(1992).
DR EMBL; M86396; AAA29866.1; -.
DR PIR; A45558; A45558.
DR HSP; P11362; IFGK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR000345; Cyt_c_heme_BS.
DR InterPro; IPR00494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00757; Furin-like; 2.
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DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00261; FU; 6.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 2.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN 1.
KW Kinase; Receptor; Signal; Transferase; Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1717 epidermal growth factor receptor.
SQ SEQUENCE 1717 AA; 192303 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1717;
Best Local Similarity 40.9%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHLHACIPQLRCS 22
DB 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 39
Q8WRP4
ID Q8WRP4 PRELIMINARY; PRT; 1476 AA.
AC Q8WRP4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase.
GN Name=MERTK1;
OS Monosiga brevicollis.
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
OX NCBI_TaxID=81824;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50154;
RX MEDLINE=21625102; PubMed=11752452;
RA King N., Carroll S.B.;
RT "A receptor tyrosine kinase from choanoflagellates: molecular insights
RT into early animal evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50154;
RX MEDLINE=22752268; PubMed=12869759;
RA King N., Hittinger C.T., Carroll S.B.;
RT "Evolution of key cell signaling and adhesion protein families
RT predates animal origins.";
RL Science 301:361-363(2003).
DR EMBL; AF440359; AAL33602.2; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00084; Sushi; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
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DR SMART; SMO0355; ZnF_C2H2; 3.  
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.  
DR PROSITE; PS01157; ZINC_FINGER_C2H2_2; 3.  
SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;  
  
Query Match 27.9%; Score 56; DB 2; Length 341;  
Best Local Similarity 29.4%; Pred.No.37;  
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 CSQNEYFDLSLTHACIPQLRCSSNTPTPLTCORYC 34  
|||::||::|||::|||::|||  
Db 60 CNEREWESQLIRSLPEHGVRCPSQLAPIPPQNYC 93  
|||||::|::|::|::|::|::|::|  
  
RESULT 41  
Q8CFA7 PRELIMINARY; PRT; 341 AA.  
ID Q8CFA7  
AC Q8CFA7  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Germ cell specific zinc finger protein.  
GN Name=Zfp393; Synonyms=Gzf;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/Sv x C57BL; TISSUE=Testis;  
RX MEDLINE=22239718; PubMed=12351194;  
RA Yan W., Burns K.H., Ma L., Matzuk M.M.;  
RT "Identification of Zfp393, a germ cell-specific gene encoding a novel  
RT zinc finger protein.";  
RL Mech. Dev. 118:233-239(2002).  
RE ENBL; AF508984; AAN31656.1; -.  
DR HSP; P08047; ISP1.  
DR MGD; MGI:2181068; Zfp393.  
DR GO; GO:0007276; P:gametogenesis; IDA.  
DR InterPro; IPR007087; Znf_C2H2.  
DR Pfam; PF000096; zf-C2H2; 3.  
DR ProDom; PD000003; Znf_C2H2; 2.  
DR SMART; SMO0355; ZnF_C2H2; 3.  
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.  
DR PROSITE; PS01157; ZINC_FINGER_C2H2_2; 3.  
SQ SEQUENCE 341 AA; 38073 MW; AC82D4C0472B054C CRC64;  
  
Query Match 27.9%; Score 56; DB 2; Length 341;  
Best Local Similarity 29.4%; Pred.No.37;  
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 CSQNEYFDLSLTHACIPQLRCSSNTPTPLTCORYC 34  
|||::||::|||::|||::|||  
Db 60 CNEREWESQLIRSLPEHGVRCPSQLAPIPPQNYC 93  
|||||::|::|::|::|::|::|::|  
  
RESULT 42  
Q9D351 PRELIMINARY; PRT; 341 AA.  
ID Q9D351  
AC Q9D351;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length enriched  
DE library, clone#742070M05 product: weakly similar to DJ675G8.1 (NOVEL  
DE ZINC FINGER PROTEIN).  
GN Name=742070M05Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF131890; AAD54072.1; -.
DR HSP; P07174; INGR.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 27.9%; Score 56; DB 2; Length 387;
Best Local Similarity 25.4%; Pred. No. 42;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOL-----RC-----SSNTPPLTQC 31
| : : : : : : : : : : : : : : : : : : : : : :
Db 103 CPERQYLDL-NGICLPQLCSKGHVVSQCTHNKNTVCQLCSGFGYSEKSSPCLPCR 161
| : : : : : : : : : : : : : : : : : : : : : :
QY 32 RYC 34
|
Db 162 TEC 164

RESULT 45
Q6NUF1
ID Q6NUF1 PRELIMINARY; PRT; 392 AA.
AC Q6NUF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC398134 protein (Fragment).
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettewen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC068640; AAH68640.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
FT NON_TER 1
SQ SEQUENCE 392 AA; 42538 MW; 0B41CED6CCE080FB CRC64;

Query Match 27.9%; Score 56; DB 2; Length 392;
Best Local Similarity 25.4%; Pred. No. 43;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOL-----RC-----SSNTPPLTQC 31
| : : : : : : : : : : : : : : : : : : : : : :
Db 108 CPERQYLDL-NGICLPQLCSKGHVVSQCTHNKNTVCQLCSGFGYSEKSSPCLPCR 166
| : : : : : : : : : : : : : : : : : : : : : :
QY 32 RYC 34
|
Db 167 TEC 169

RESULT 46
AAH68640
ID AAH68640 PRELIMINARY; PRT; 392 AA.
AC AAH68640;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC398134 protein (Fragment).
GN LOC398134.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettewen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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FT CARBOHYD 1843 1843 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1965 1965 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2122 2122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2165 2165 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2178 2178 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2329 2329 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2359 2359 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 823 823 C -> V (in Ref. 1; AA sequence).
 FT CONFLICT 923 923 S -> Y (in Ref. 1; AA sequence).
 FT CONFLICT 965 965 W -> Y (in Ref. 1; AA sequence).
 FT CONFLICT 1241 1241 S -> K (in Ref. 1; AA sequence).
 SQ SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;

Query Match 27.9%; Score 56; DB 1; Length 2476;
 Best Local Similarity 31.6%; Pred. NO. 2.9e+02;
 Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 1 CSQNEYFDLSLHACIP-CQ---LRCSSNTPPLTCQRYC 34
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1851 CSAHSVYTSVPSCLPSCQDPGEGCTGAGAPSTCEEGC 1888

RESULT 48

Q9EP28 PRELIMINARY; PRT; 146 AA.

AC Q9EP28;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polyprotein (fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinzawa H., Shao L., Jiang Q., Togaishi H., Zhang X., Ihibashi M.,
 RA Watanabe H., Saito T., Takahashi T., Ohba K., Mizokami M.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB030968; BAB11770.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR002519; HCV env.
 DR Pfam: PF01539; HCV env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON TER 1 1
 FT NON TER 146 146
 SQ SEQUENCE 146 AA; 15763 MW; 9C67046FD8507C30 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 146;
 Best Local Similarity 31.8%; Pred. NO. 18;
 Matches 14; Conservative 6; Mismatches 13; Indels 11; Gaps 3;

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 Db 34 CSNSNITWLTDAVHLHFGVPCPSDNGTLRCWQVTPNAVY 77

RESULT 49

Q9VE40 PRELIMINARY; PRT; 225 AA.

AC Q9VE40;
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 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG7714-PA (RH24988p).
 GN ORFNames=CG7714;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Balswin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
 RA Nelson D.B., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; and
 RT "finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomes perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.B., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:36:38 ; Search time 9.04587 Seconds
(without alignments)
249.264 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41
Perfect score: 201
Sequence: 1 CSQNEVFDLLHACIPQLRCSSNTPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	34	4 US-09-854-864-7	Sequence 7, Appli
2	201	100.0	51	4 US-09-854-864-6	Sequence 6, Appli
3	201	100.0	58	4 US-09-854-864-21	Sequence 21, Appli
4	201	100.0	81	4 US-09-854-864-13	Sequence 13, Appli
5	201	100.0	181	4 US-09-854-864-5	Sequence 5, Appli
6	201	100.0	184	4 US-09-854-864-11	Sequence 11, Appli
7	201	100.0	283	4 US-09-854-864-9	Sequence 9, Appli
8	136	67.7	185	4 US-09-854-864-17	Sequence 17, Appli
9	136	67.7	185	4 US-09-854-864-11	Sequence 11, Appli
10	136	67.7	281	4 US-09-854-864-10	Sequence 10, Appli
11	93.5	46.5	117	4 US-09-854-864-12	Sequence 12, Appli
12	66.5	33.1	59	4 US-09-854-864-20	Sequence 20, Appli
13	66.5	33.1	67	4 US-09-854-864-16	Sequence 16, Appli
14	66.5	33.1	166	2 US-08-810-572A-6	Sequence 6, Appli
15	66.5	33.1	166	3 US-09-290-333-6	Sequence 6, Appli
16	66.5	33.1	166	4 US-09-782-857A-6	Sequence 6, Appli
17	66.5	33.1	166	4 US-09-854-864-15	Sequence 15, Appli
18	66.5	33.1	293	2 US-08-810-572A-2	Sequence 2, Appli
19	66.5	33.1	293	3 US-09-290-333-2	Sequence 2, Appli
20	66.5	33.1	293	4 US-09-782-857A-2	Sequence 2, Appli
21	66.5	33.1	293	4 US-09-879-919-22	Sequence 22, Appli
22	66.5	33.1	293	4 US-09-848-295-4	Sequence 4, Appli
23	66.5	33.1	293	4 US-09-854-864-14	Sequence 14, Appli
24	66.5	33.1	397	4 US-09-854-864-18	Sequence 18, Appli
25	56	27.9	2476	2 US-08-276-967-2	Sequence 2, Appli
26	54	26.9	98	4 US-09-621-976-6330	Sequence 6330, Ap
27	54	26.9	431	4 US-09-252-991A-25721	Sequence 25721, A

28	53.5	26.6	381	3	US-09-257-580-2	Sequence 2, Appli
29	53.5	26.6	5405	3	US-08-718-388-9	Sequence 9, Appli
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32	52	25.9	624	4	US-09-877-730-24	Sequence 24, Appli
33	52	25.9	712	4	US-09-877-730-22	Sequence 22, Appli
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35	52	25.9	904	4	US-09-877-730-6	Sequence 6, Appli
36	52	25.9	991	4	US-09-877-730-12	Sequence 12, Appli
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41	51.5	25.6	77	2	US-08-465-380-4	Sequence 4, Appli
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49	51.5	25.6	77	2	US-08-461-965-40	Sequence 40, Appli
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51	51.5	25.6	77	2	US-08-634-641-4	Sequence 4, Appli
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53	51.5	25.6	77	3	US-09-249-471-4	Sequence 4, Appli
54	51.5	25.6	77	3	US-09-249-471-40	Sequence 40, Appli
55	51.5	25.6	77	3	US-09-249-472-4	Sequence 4, Appli
56	51.5	25.6	77	3	US-09-249-472-40	Sequence 40, Appli
57	51.5	25.6	77	3	US-09-249-451-4	Sequence 4, Appli
58	51.5	25.6	77	3	US-09-249-451-40	Sequence 40, Appli
59	51.5	25.6	77	3	US-08-809-455-4	Sequence 4, Appli
60	51.5	25.6	77	3	US-08-809-455-40	Sequence 40, Appli
61	51.5	25.6	77	3	US-09-249-461-4	Sequence 4, Appli
62	51.5	25.6	77	3	US-09-249-461-40	Sequence 40, Appli
63	51.5	25.6	77	3	US-09-249-448-4	Sequence 4, Appli
64	51.5	25.6	77	3	US-09-249-448-40	Sequence 40, Appli
65	51.5	25.6	77	4	US-09-249-473-4	Sequence 4, Appli
66	51.5	25.6	77	4	US-09-249-473-40	Sequence 40, Appli
67	51.5	25.6	81	2	US-08-465-380-7	Sequence 7, Appli
68	51.5	25.6	81	2	US-08-480-478-36	Sequence 36, Appli
69	51.5	25.6	81	2	US-08-486-397-7	Sequence 7, Appli
70	51.5	25.6	81	2	US-08-486-399-7	Sequence 7, Appli
71	51.5	25.6	81	2	US-08-461-965-7	Sequence 7, Appli
72	51.5	25.6	81	2	US-08-326-110A-36	Sequence 36, Appli
73	51.5	25.6	81	2	US-08-634-641-7	Sequence 7, Appli
74	51.5	25.6	81	3	US-09-249-471-7	Sequence 7, Appli
75	51.5	25.6	81	3	US-09-249-472-7	Sequence 7, Appli
76	51.5	25.6	81	3	US-09-249-451-7	Sequence 7, Appli
77	51.5	25.6	81	3	US-08-809-455-7	Sequence 7, Appli
78	51.5	25.6	81	3	US-09-249-461-7	Sequence 7, Appli
79	51.5	25.6	81	3	US-09-249-448-7	Sequence 7, Appli
80	51.5	25.6	81	4	US-09-249-473-7	Sequence 7, Appli
81	51.5	25.6	100	2	US-08-465-380-20	Sequence 20, Appli
82	51.5	25.6	100	2	US-08-480-478-48	Sequence 48, Appli
83	51.5	25.6	100	2	US-08-486-397-20	Sequence 20, Appli
84	51.5	25.6	100	2	US-08-486-399-20	Sequence 20, Appli
85	51.5	25.6	100	2	US-08-461-965-20	Sequence 20, Appli
86	51.5	25.6	100	2	US-08-326-110A-48	Sequence 48, Appli
87	51.5	25.6	100	2	US-08-634-641-20	Sequence 20, Appli
88	51.5	25.6	100	3	US-09-249-471-20	Sequence 20, Appli
89	51.5	25.6	100	3	US-09-249-472-20	Sequence 20, Appli
90	51.5	25.6	100	3	US-09-249-451-20	Sequence 20, Appli
91	51.5	25.6	100	3	US-08-809-455-20	Sequence 20, Appli
92	51.5	25.6	100	3	US-09-249-461-20	Sequence 20, Appli
93	51.5	25.6	100	3	US-09-249-448-20	Sequence 20, Appli
94	51.5	25.6	100	4	US-09-249-473-20	Sequence 20, Appli
95	51.5	25.6	192	1	US-08-086-428B-81	Sequence 81, Appli
96	51.5	25.6	192	2	US-08-468-570-81	Sequence 81, Appli
97	51.5	25.6	192	2	US-08-290-665A-81	Sequence 81, Appli
98	51.5	25.6	192	4	US-08-466-601A-81	Sequence 81, Appli
99	51.5	25.6	192	5	PCT-US95-10398-81	Sequence 81, Appli
100	51.5	25.6	282	4	US-09-544-618-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 100.0%; Score 201; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34

RESULT 2
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 100.0%; Score 201; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 38

RESULT 3
US-09-854-864-21

; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 100.0%; Score 201; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34

RESULT 4
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34

RESULT 5
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 38

RESULT 6

US-09-565-423-11
Sequence 11, Application US/09565423
Patent No. 6475987
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 7

US-09-854-864-9
Sequence 9, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 100.0%; Score 201; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 38

RESULT 8

US-09-565-423-17
Sequence 17, Application US/09565423
Patent No. 6475987
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 185
TYPE: PRT
ORGANISM: Mus musculus
US-09-565-423-17

Query Match 67.7%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. No. 6.4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSNTPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 9

US-09-854-864-11
Sequence 11, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 185
TYPE: PRT
ORGANISM: Murine
US-09-854-864-11

Query Match 67.7%; Score 136; DB 4; Length 185;

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Best Local Similarity 70.6%; Pred. No. 6.4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 10
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 4; Length 281;
Best Local Similarity 70.6%; Pred. No. 9.6e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 11
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 46.5%; Score 93.5; DB 4; Length 117;
Best Local Similarity 65.7%; Pred. No. 0.00044;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

Qy 2 SONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
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```
RESULT 12
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 33.1%; Score 66.5; DB 4; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.35;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAFPC 33

RESULT 13
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match 33.1%; Score 66.5; DB 4; Length 67;
Best Local Similarity 32.4%; Pred. No. 0.4;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAFPC 33

RESULT 14
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
```



```

/ TELEFAX: 201-343-1684
/
/ INFORMATION FOR SEQ ID NO: 6:
/
/ SEQUENCE CHARACTERISTICS:
/
/   LENGTH: 166 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/
/   MOLECULE TYPE: peptide
/   HYPOTHETICAL: NO
/   FRAGMENT TYPE: N-terminal
/   ORIGINAL SOURCE:
/
/     ORGANISM: Homo sapiens
/
/   SEQUENCE DESCRIPTION: SEQ ID
/ US-09-782-857A-6

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Query Match      33.1%; Score 66.5; DB 4; Length 166;
Best Local Similarity 32.4%; Pred.No. 0.96;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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RESULT 17
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

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Query Match      33.1%; Score 66.5; DB 4; Length 166;
Best Local Similarity 32.4%; Pred.No.0.96;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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RESULT 18
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack

STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 33.1%; Score 66.5; DB 2; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Gaps 1;

RESULT 19
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

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; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-782-857A-2
```

Query Match Best Local Similarity Matches 11;	33.1%; Score 66.5; DB 4; Pred No. 1.7; Mismatches 8; Conservative
Length 293; Indels 1; Gaps 1;	

QY 1 CSONEFYFDSLHACIPCQLRCSNTPTPLTCORYC 34
 | : : | | | | : : : : | : : |
Db 34 CPBEQWDPLLGTSCSKTICNHQS-QRTCAAFc 66

```
RESULT 21  
US-09-879-919-22  
; Sequence 22, Application US/09879919  
; Patent No. 6541224  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: PF253PI  
; CURRENT APPLICATION NUMBER: US/09/879,919  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254,875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241,952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211,537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815,783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016,812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-879-919-22
```

Query Match Best Local Similarity Matches 11;	33.1%; Score 66.5; DB 4; Pred No. 1.7; Mismatches 8; Conservative
Length 293; Indels 1; Gaps 1;	

QY 1 CSONEFYFDSLHACIPCQLRCSNTPTPLTCORYC 34
 | : : | | | | : : : : | : : |
Db 34 CPBEQWDPLLGTSCSKTICNHQS-QRTCAAFc 66

```
RESULT 22  
US-09-848-295-4  
; Sequence 4, Application US/09848295  
; Patent No. 6623941  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon  
; FILE REFERENCE: PF527  
; CURRENT APPLICATION NUMBER: US/09/848,295  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/202,193  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1
```

```
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 23
US-09-854-864-14
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 24
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      33.1%; Score 66.5; DB 4; Length 397;
```

```
Best Local Similarity 32.4%; Pred. No. 2.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 25
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2

Query Match      27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.8%; Pred. No. 2.3e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-CQ---LRCSSNTPPLTCQRYC 34
Db 1851 CSAHSVYVTSVPSCLPSCQDPGQCTGAGAPSTCEGC 1888

RESULT 26
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
```



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; SOFTWARE: Patent.pm
; SEQ ID NO 6330
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6330

Query Match      26.9%; Score 54; DB 4; Length 98;
Best Local Similarity 38.1%; Pred. No. 17;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 14 CIPQLRCSNTPLTCQRYC 34
:||||:||||:|
Db 58 CLPCPSQSPSCPPQPCCKPC 78

RESULT 27
US-09-252-991A-25721
; Sequence 25721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25721
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25721

Query Match      26.9%; Score 54; DB 4; Length 431;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 13 ACIPQLRCSNTPLTCQRYC 32
:||||:||||:|
Db 242 AC--CRARCSNAWPPTACRR 259

RESULT 28
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2

Query Match      26.6%; Score 53.5; DB 3; Length 381;
Best Local Similarity 48.3%; Pred. No. 74;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

Qy 4 NEYFDSLHACICPQLRCSNTPLTCQRYC 32
:||||:||||:|
Db 2733 CPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763

RESULT 29
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAKKI
; TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-388-9

Query Match      26.6%; Score 53.5; DB 3; Length 5405;
Best Local Similarity 34.3%; Pred. No. 9.8e+02;
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

Qy 1 CSQNEYFDSLHACI-PCQLRCSNTPLTCQRYC 34
:||||:||||:|
Db 2733 CPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763

RESULT 30
US-09-848-295-2
; Sequence 2, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
```


QY 4 NEYFDSLHACIPQLRCSSTNPPLTCQRY 33
 | : | : | : | : | : | : | : |
D6 782 NSFIDAKVLSGIGICISRSSIPPCCVKMY 811

```

RESULT 35
US-09-877-730-6
; Sequence 6, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Pl
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6

```

```

RESULT 36
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Pl
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

```

```

RESULT 37
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. 6465632el Human Phosph
; FILE REFERENCE: LEX-0189-US
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

```

RESULT 38
US-08-117-080-12
Sequence 12, Application US/08117080
Patent No. 5482928
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKART, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARRY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,080
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSSNT-PPLTCQRYC 34
Db 24 MIEACIGNGRGNENVGPPYCCSGFC 49

RESULT 39

US-08-471-329-12
Sequence 12, Application US/08471329
Patent No. 5689048
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,329
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-471-329-12
Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
Qy 10 LLHACIPQLRCSSNT-PPLTCQRYC 34
Db 24 MIEACIGNGRGNENVGPPYCCSGFC 49

RESULT 40

US-08-915-142-12
Sequence 12, Application US/08915142
Patent No. 5942663
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,142
FILING DATE: 20-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,329
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-915-142-12

	TITLE OF INVENTION:	NEMATODE-EXTRACTED ANTI-
:		:
	TITLE OF INVENTION:	COAGULANT PROTEIN
:		:

```
/
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: California
/ ZIP: 90071
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSEQ Version 1.5
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,478
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/326,110
/ FILING DATE: 18 OCTOBER 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BIGGS, SUZANNE L.
/ REGISTRATION NUMBER: 30,158
/ REFERENCE/DOCKET NUMBER: 208/290
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 77 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/
/ US-08-480-478-33
/
/ Query Match 25.6%; Score 51.5; DB 2; Length 77;
/ Best Local Similarity 29.3%; Pred. No. 27;
/ Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
/
/ QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34
/ Db 6 CGENWLDD-----CGTQKPCCAKNCBPPPEEDPICRSRG 42
/
/ RESULT 44
/ US-08-486-397-4
/ Sequence 4, Application US/08486397
/ Patent No. 5866542
/ GENERAL INFORMATION:
/ APPLICANT: George P. Vlasuk, Patric H. Stanssens,
/ APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
/ APPLICANT: Yves R. Laroche, Laurent S. Jespers,
/ APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
/ APPLICANT: Peter W. Bergum
/ TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
/ NUMBER OF SEQUENCES: 357
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: U.S.A.
/ ZIP: 90071
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,478
/ FILING DATE: June 5, 1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/326,110
/ FILING DATE: October 18, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BIGGS, SUZANNE L.
/ REGISTRATION NUMBER: 30,158
/ REFERENCE/DOCKET NUMBER: 213/269
/ TELECOMMUNICATION INFORMATION:
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,397
/ FILING DATE: June 5, 1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/326,110
/ FILING DATE: October 18, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BIGGS, SUZANNE L.
/ REGISTRATION NUMBER: 30,158
/ REFERENCE/DOCKET NUMBER: 213/269
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 77 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Ancylostoma caninum
/
/ US-08-486-397-4
/
/ Query Match 25.6%; Score 51.5; DB 2; Length 77;
/ Best Local Similarity 29.3%; Pred. No. 27;
/ Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
/
/ QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34
/ Db 6 CGENWLDD-----CGTQKPCCAKNCBPPPEEDPICRSRG 42
/
/ RESULT 45
/ US-08-486-397-40
/ Sequence 40, Application US/08486397
/ Patent No. 5866542
/ GENERAL INFORMATION:
/ APPLICANT: George P. Vlasuk, Patric H. Stanssens,
/ APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
/ APPLICANT: Yves R. Laroche, Laurent S. Jespers,
/ APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
/ APPLICANT: Peter W. Bergum
/ TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
/ NUMBER OF SEQUENCES: 357
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: U.S.A.
/ ZIP: 90071
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,397
/ FILING DATE: June 5, 1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/326,110
/ FILING DATE: October 18, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BIGGS, SUZANNE L.
/ REGISTRATION NUMBER: 30,158
/ REFERENCE/DOCKET NUMBER: 213/269
/ TELECOMMUNICATION INFORMATION:
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03-08-780-332-4

US-08-461-965-4

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; Sequence 4, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-461-965-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD----CGTQKPCAKCNEPPEEDPICRSRG 42

RESULT 49
US-08-461-965-40
; Sequence 40, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-461-965-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD----CGTQKPCAKCNEPPEEDPICRSRG 42

RESULT 50
US-08-326-110A-33
; Sequence 33, Application US/08326110A
; Patent No. 5945275
; GENERAL INFORMATION:
; APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
; APPLICANT: HUGO STANSSENS; JORIS HILDA
; APPLICANT: LIEVEN MESSENS; MARC JOZEF
; APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
; APPLICANT: LAURENT STEPHANE JESPEERS; and
; APPLICANT: YANNICK GEORGES JOZEF
; APPLICANT: GANSEMAN
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
; TITLE OF INVENTION: COAGULANT PROTEIN
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
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